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(64) Recombinant antibodies specific for a growth factor receptor.

(iii) The invention concerns recombinant antibodies directed to the extracellular domain of the human growth factor receptor cerbia-2 comprising a light chain variable domain and a heavy chain variable domain of a monocional antibody, monocional antibodies directed to cerbia-2 themselves, a method of manufacture of said recombinant antibodies and said monocional antibodies, a prethod of manufacture of said hybridoran cells, DNA coding for the heavy chain variable domain, for the light chain variable domain and for the recombinant antibody, a method of manufacture of said DNA, phorif vectors suitable for expression of said DNA, host cells transformed with said DNA, and the use of said recombinant antibodies and said monocional antibodies in the diagnosis and treatment of humors.

Background of the invention

Growth factors and their receptors are involved in the regulation of cell proliferation, and they also seem to play a role in tumor growth. The cerbB-2 growth factor receptor protein, a protein of the membrane receptor protein tyrosine kinase family (A. Ulrich & J. Schlessinger, Cell 61: 203-212, 1990), is found in human breast tumors and human ovarian carcinomas. Amplification of the cerbB-2 green and over-expression of the protein tumors and human ovarian carcinomas. Amplification of the cerbB-2 protein has potential, both as a diagnostic marker and as a target for cancer therapy. Sequence analysis reveals that cerbB-2, also called EFR2, a glycoprotein of 195 kino-Dalton (pg 193), is identical or closely related to the human analog of the neu oncogene (A.L. Schechter et al., Science 229: 976-978, 1985) and shows considerable sequence homology to the human availage tor (FGF) receptors.

Of particular interest in tumor diagnosis and therapy are antibodies directed to tumor markers. Polydonal antibodies may be obtained from the serum of marmanels immunized with the antigen, Le, the tumor marker. The development of hybridoma technology made it possible to generate continuous cell lines, in particular murine hybridomas, producing monocional antibodies of the desired specificity. Murine monocional antibodies directed to certifical, experience and are described, for example, by Specificity. Murine monocional antibodies directed to certifical experience and are described, for example, by SJ. Mickenzie et al., Oncogenet 6:435-348, 1989; R.M.Hudziak et al., Molecular and Cellular Biology 9: 1165-1172, 1989; International Patent Application WO 89/06892 (Genentech); and Japanese Patent Application Kokai Q2:160293 (Ajinomoto KK).

A promising alternative is the modification of immunoglobulin genes in order to tailor antibodies for particular diagnostic and therapeutic tasks. Due to the fact that the variable region and each of the constant region domains of immunoglobulin molecules are encoded in separate exons with their own splice sites, recombinant DNA techniques can be used to isolate different parts of cloned immunoglobulin genes and ligate them to parts of other immunoglobulins or to effector molecules. The reconstructed genes are expressed by appropriate transformed continuous cell lines. Murine antibodies can, for example, be converted into "humanized" antibodies by exchanging murine constant domain exons for human immunoglobulin constant domain exons, thus generating chimeric antibodies with murine antibody-combining sites and human constant domains. The chimeric antibodies retain the antigen specificity determined by the murine variable domains, but also exhibit human effector functions (such as complement binding, stimulation of phagocytosis, triggering of granule release by mast cells) determined by the carboxy-terminal constant domain segments of the heavy chain polypeptides. An even more sophisticated technique in tailoring antibodies described in European Patent Application 0 239 400 exchanges also other fairly conserved domains, the so-called framework regions (FRs), within the murine variable domains for corresponding framework regions from human antibodies or for other human protein sequences. Such an antibody should be even less immunogenic in man since the only parts derived from a murine antibody are those hypervariable regions which define a particular specificity for an antigen, the so-called complementarity determining regions (CDRs).

Furthermore, fusion proteins different from immunoglobulins may be formed, e.g. single-chain antibodies, which ratian the specificity and binding properties of the starting murine monoclonal antibody. but have otherwise novel properties derived from the non-immunoglobulin part of the fusion protein. The smallest domain of a monoclonal antibody which can bind to the antigen is the so-called Fv fragment which consists of the variable domains of the heavy and light chains. Fv fragments are difficult to prepare by proteolytic techniques since the corresponding variable domains tend to dissociate upon diution. Fv midecules constructed by joining the variable domains of the heavy and light chains via a short peptide linker, also called single-chain antigen binding proteins, bind to an antigen with similar characteristics as the original monoclonal antibody (R.E. Bird et al., Science 242-2426, 1988; J.S.Huston et al., Proc. Natl. Acad. Sci. USA 85: 5879-5883, 1985; and International Patent Application WO 89/09825 (Celltech)). Fv encoding genes can, in principle, be linked to genes encoding effector molecules by recombinant gene technology, It is known, for example, that Fv encoding gene sequences can be linked to a gene encoding a portion of the <u>Pseudomonas</u> exotoxin A gene (V.K. Chaudhary et al., Natura 393: 394-397, 1998; and International Patent Application WO 89/11933, Q. Passian et al.)).

Object of the invention

It is an object of this invention to provide recombinant antibodies directed to the extracellular domain of the human growth factor receptor c-erbB-2 comprising a light chain variable domain and a heavy chain variable domain of a monoclonal antibody, monoclonal antibodies directed to c-erbB-2 themselves, a method of manufacture of said recombinant antibodies and said monoclonal antibodies, hybridoma cells secreting said monoclonal antibodies, a method of manufacture of said hybridoma cells, DNA coding for the heavy chain variable domain, for the light chain variable domain and for the recombinant antibody, a method of manufacture of said DNA, hybrid vectors suitable for expression of said DNA, host cells transformed with said DNA, and the use of said recombinant antibodies and said monoclonal antibodies in the diagnosis and treatment of tumors.

Detailed description of the invention

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The invention concerns a recombinant antibody directed to the extracellular domain of the growth factor receptor c-eraB-2, a human glycoptotein of 185 kilo-Dalton (gp185), comprising a heavy chain variable domain and a light chain variable domain of a monoclonal antibody.

Such a recombinant antibody may be a chimeric antibody consisting, for example, of a mouse heavy chain variable domain with the specificity for cerbB-2 and a human heavy chain constant domain $\alpha, \gamma, \delta, s, \sigma \mu, preferably, such as <math>\gamma 1$ or $\gamma 4$, and of a mouse light chain variable domain with the specificity for cerbB-2 and a human light chain constant domain κ or λ , referably κ , all assembled to olive a functional antibody.

The preferred recombinant antibody of the invention is a single-chain antibody wherein the heavy chain valieb domain and the light chain variable domain and the light chain variable domain and the light chain variable domain and the light chain variable. Most preferred is a single-chain antibody wherein the heavy chain variable domain is located at the N-terminus of the recombinant antibody. The single-chain recombinant antibody may further comprise an effector molecule and or signal sequences facilitating the processing of the antibody by the host cell in which it is prepared. Effector molecules considered are those useful for diagnosities or therapeutic purposes, for example enzymes causing a detectable reaction, e.g., phosphatases, use as alkaline phosphatases from Ecolor or manualina sikaline phosphatase, e.g. bovine alkaline phosphatase, horeardish percodase, β-D-galactosidase, glucose oxidase, glucosmylases, carbonic anhylvrase, acetylcholinesterase, lyozyme, malate dehydrogenase or glucoses-phosphate, a peptide having particular binding properties, e.g. streptavidin from Streptomyces avidinii strongly binding to biolin, or enzymes, toxins or other drugs attacking the cells to which the antibody is bound, e.g. a protease, a cytolysin or an excloxin, for example ricin A, diphtheria toxin A, or Pseudomonas exotoxin. In the following a single-chain recombinant antibody further comprising an effector molecule is referred to as fusion protein or intended to be within the meaning of the terms "single chain (recombinant) antibody" or "recombinant antibody" and proteins and the protein and the protein or intended to be within the meaning of the terms "single chain (recombinant) antibody" or "recombinant antibody" and proteins and the protein and the protein or intended to be within the meaning of the terms "single chain (recombinant) antibody" or "recombinant antibody" and proteins and the protein and t

The term effector molecule also includes biologically active varients of the above-metrioned protains, e.g., variants produced from a DNA which has been subjected to <u>in vito</u> mutagenesis, with the provision that the protein encoded by said DNA retains the biological activity of the native protein. Such modifications may consist in an addition, exchange or deletion of amino acids, the latter resulting in shortened variants. For example, an enzyme, such as phosphatases, may be prepared from a DNA which has been modified to facilitate the cloning of the encoding gene, or an exotoxin, such as Pseudomonas exotoxin, may be prepared from a DNA which has been mutated to delete the cell binding domain.

The recombinant antibodies of the Invention are tested for their specificity to the extracellular domain of c-erbB-2, for example by immunofluorescent statining of cells spyressing high levis of c-erbB-2, by immunoblotting either directly or by way of immunoprecipitation and protein blotting of the immunocomplexes, or by another immunosassa yeuch as a binding, crossinshibition or commedition radio- or enzyme immunosassa.

The variable domain of an antibody heavy or light chain consists of so-called framework regions (FRs), which are fairly conserved in antibodies with different specificities, and of hypervariable regions also called complementarity determining regions (CDRs), which are typical for a particular specificity.

Preferred recombinant antibodies of the invention are those wherein the heavy chain variable domain comprises a polypeptide of the formula

FR, -CDR₁₀-FR₂-CDR₃₀-FR₄ (I)

wherein FR, is a polypeptide residue comprising at least 25-29, preferably 25-33 naturally occurring amino acids, FR₂ is a polypeptide residue comprising 12-16 naturally occurring amino acids, FR₃ is a polypeptide residue comprising 9.34 naturally occurring amino acids, FR₄ is a polypeptide residue comprising at least 6-10, preferably 6-13 naturally occurring amino acids, CDR_{1W} is a polypeptide residue of the amino acid sequence

32 to 36 of SEQ ID NO:4, CDR $_{2H}$ is a polypeptide residue of the amino acid sequence 51 to 67 of SEQ ID NO:4, and CDR $_{3H}$ is a polypeptide residue of the amino acid sequence 100 to 109 of SEQ ID NO:4, or, CDR $_{1H}$ is a

polypeptide residue of the amino acid sequence 32 to 38 of SEQ ID NO.8, CDR_{2n} is a polypeptide residue of the amino acid sequence 51 to 67 of SEQ ID NO.8, and CDR_{2n} is a polypeptide residue of the amino acid sequence 100 to 110 of SEQ ID NO.8, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges. These particular complementarity determining regions are Asn-Tyr-Gly-Met-Asn (CDR_{2n}), Trp-Ile-Asn-Thr-Ser-Tin-Tin-Gly-Glu-Ser-Tin-Phe-Ala-Asp-Asp-Phe-Lys-Gly (CDR_{2n}), and Trp-Glu-Val-Tyr-His-Gly-Tyr-Val-Pro-Tyr (CDR_{2n}) according to SEQ. ID NO.4, or Ser-Tyr-Tyr-Met-Asn (CDR_{2n}), Met-Ile-Asp-Pro-Ser-Asp-Ser-Glu-Tir-Gln-Tyr-Asn-Glm-Met-Phe-Lys-Asp (CDR_{2n}) and Gly-Gly-Ala-Ser-Gly-Asp-Tip-Tyr-Phe-Asp-Val (CDR_{2n}) according to SEO. ID NO.8.

Especially preferred are recombinant antibodies comprising a heavy chain variable domain of formula I, wherein the polypeptide residues of the framework regions FR₄, FR₂, FR₃ and FR₄ are those preferably occurring in mammalian, especially murine or human, antibodies.

In a first embodiment of the invention, most preferred are recombinant antibodies with a heavy chain variable domain comprising a polypeptide of the amino acid sequence 2 to 120, of SEQ ID NOA. Wherein optionally one or more, e.g. 1, 2, 3 or 4, single amino acids within the amino acid sequences 2 to 31 (FR₁), 37 to 50 (FR₂), 83 to 39 (FR₃), and/or 110 to 120 (FR₃), are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-5-bridges, in particular the recombinant antibodies with a heavy chain variable domain comprising a polypeptide of the amino acid sequence 2 to 120 of SEQ ID NO:4, wherein the amino acid Cys may be in the oxidized state forming S-5-bridges.

In a second embodiment of the invention, most preferred are recombinant antibodies wherein the heavy chain variable domain comprises a polypeptide of the arimo acid sequence 2 to 12(, of SEQ ID NO; 8, wherein optionally one or more, e.g. 1, 2, 3 or 4, single amino acids within the amino acid sequences 2 to 31 (FR₁), 37 to 50 (FR₉), 8 to 99 (FR₉), and/or 1110 121 (FR₁), are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-3-bridges, in particular the recombinant antibodies with a heavy chain variable domain comprising a polypeptide of the amino acid sequence 2 to 121 of SEQ ID NO; 8, wherein the amino acid Cys may be in the oxidized state forming S-3-bridges.

For example, a hydrophobic amino acid within the framework regions may be replaced by another amino acid, preferably also a hydrophobic amino acid, e.g. a homologous amino acid, replaced by two amino acids or deleted. Likewise, a hydrophobic amino acid within the framework region may be replaced by another amino acid, two amino acids or deleted, whereby replacing amino acids preferably maintain the hydrogen bond structure of the corresponding framework region.

Likewise preferred recombinant antibodies of the invention are those wherein the light chain variable domain comprises a polypeptide of the formula

wherein FR, is a polypeptide residue comprising naturally occurring amino acids, preferably 19-25, especially 19-23 naturally occurring amino acids, FR, is a polypeptide residue comprising 13-17 naturally occurring amino acids, FR, is a polypeptide residue comprising 13-17 naturally occurring amino acids, FR₆ is a polypeptide residue comprising naturally occurring amino acids, and CRR₁, is a polypeptide residue of the amino acid sequence 158 to 191 of 35EQ in NO-4, CDR₂, is a polypeptide residue of the amino acid sequence 158 to 191 of 35EQ in NO-4, and CDR₂, is a polypeptide residue of the amino acid sequence 168 to 191 of 35EQ in NO-4, and CDR₂, is a polypeptide residue of the amino acid sequence 169 to 190 NO-4, or CDR₂, is a polypeptide residue of the amino acid sequence 169 to 192 of 35EQ in NO-8, and CDR₂, is a polypeptide residue of the amino acid sequence 169 to 192 of 35EQ in NO-8, and CDR₂, is a polypeptide residue of the amino acid sequence 168 to 192 of 35EQ in NO-8, and CDR₂, is a polypeptide residue of the amino acid sequence 25 to 232 of 35EQ in NO-8, and wherein the amino acid Cys may be in the oxidized state forming S-5-bridges. These particular complementarity determing regions are Lys-Ala-Ser-Gin-Aap-Val-Tyr-Ann-Ala-Val-Ala (CDR₁), Ser-Ala-Ser-Ser-Arg-Tyr-Thr (CDR₂), and Gin-Gin-His-Phe-Arg-Tin-Pho-Phe-Thr (CDR₂) according to 35EQ in No-8, or Lys-Ala-Ser-Gin-Asp-Ile-Lys-Lys-Tyr-Ile-Ala (CDR₁), Tyr-Thr-Ser-Val-Leu-Gin-Pro (CDR₂) and Leu-His-Tyr-Asp-Tyr-Leu-Tyr-Thr (CDR₂) according to 35EQ in No-8.

Especially preferred are recombinant antibodies comprising a light chain variable domain of formula II, wherein the polypeptide residues of the framework regions FR₆, FR₆, FR₇ and FR₈ are those preferably occurring in mammalian, especially murine or human, antibodies.

In one embodiment of the invention, most preferred are recombinant ambbodies wherein the light chain variable domain comprises a polypeptide of the amino and sequence 136 to 241 of SEQ ID NO.4, wherein optionally one or more, e.g. 1, 2, 3 or 4, single amino acide within the amino acid sequences 138 to 158 (FR_a), 170 to 184 (FR_b), 192 to 223 (FR_b), and/or 235 to 241 (FR_b) are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-b-fridges, In particular the recombinant antibodies with a light chain variable domain comprising a polypeptide of the amino acid designence 136 to 241 of SEQ ID NO.4, wherein the amino acid Cys may be in the oxidized state forming S-b-fridges.

In a second embodiment of the invention, most preferred are recombinant antibodies wherein the light chain

variable domain comprises a polypeptide of the amino acid sequence 137 to 241 of SEQ ID NO:8, wherein optionally one or more, e.g. 1, 2, 3 or 4 single amino acids within the amino acid sequences 137 to 159 (FRs), 171 to 185 (FR₂), 193 to 224 (FR₈), and/or 233 to 241 (FR₉) are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges, in particular the recombinant antibody wherein the light chain variable domain comprises a polypeptide of the amino acid sequence 137 to 241 of SEQ ID NO:8, wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.

For example, amino acids within the framework regions may be replaced by other amino acids or deleted as detailed above for the heavy chain.

Especially preferred is a single-chain recombinant antibody wherein the heavy chain variable domain and the light chair variable domain are linked by way of a spacer group consisting of 10 to 30, e.g. around 15, amino acids, in particular a single-chain recombinant antibody comprising a polypeptide of the formula

FR₁-CDR_{1H}-FR₂-CDR_{2H}-FR₃-CDR_{3H}-FR₄-CDR_{3H}-FR₄-CDR_{3H}-FR₅-CDR_{3H}-FR_{5H}-CDR_{3H}-FR wherein FR1,CDR1H,FR2,CDR2H,FR3,CDR3H,FR4,FR4,CDR1L,FR7,CDR2L, FR8,CDR3L and FR3 have the meanings as mentioned before and Sp is a peptide spacer consisting of about 10 to 30, e.g. around 15, amino acids; and wherein the heavy chain or the light chain variable domain is further connected to an effector molecule,

e.g. an enzyme, such as phosphatase, particularly alkaline phosphatase, or a toxin, such as Pseudomonas exotoxin, or a variant thereof. Preferably, the effector molecule is connected to the light chain variable domain. optionally via a peptide spacer consisting of one or more, e.g. 1-10 amino acids.

These fusion proteins comprising a single-chain recombinant antibody and an effector molecule optionally comprise another peptide, e.g. a peptide facilitating purification, in particular a peptide being an epitope against which an antibody is available, such as the FLAG peptide. Purification, e.g. by means of affinity chromatography, of a fusion protein comprising such a peptide is advantageous e.g. in that it may be faster, more specific and/or gentler. The peptide may be placed at the N-terminus of the fusion protein, in between the recombinant antibody and the effector molecule, or at the C-terminus of the fusion protein. Preferably, it is located at the N-terminus or at the C-terminus, in particular at the N-terminus. Preferably, these constructs also contain a cleavage site, so that the fusion protein can be liberated therefrom, either by enzymatic cleavage. e.g. by enterokinase or by Factor Xa, or by the chemical methods known in the art. Furthermore these constructs may comprise a peptide spacer consisting of one or more, e.g. 1 to 10, in particular about 2 amino acids, said spacer facilitating the linkage of the above-mentioned peptide and/or the cleavage site to the recombinant antibody. The cleavage site is placed in such a way that the fusion protein comprising the recombinant antibody and the effector molecule can be easily liberated, if desired, preferably in vitro. For example, in the protein construct comprising the fusion protein designated Fv(FRP5)-ETA (cf. SEQ. ID NO: 10), the FLAG peptide and an enterokinase cleavage site are linked to a spacer and placed in front of the Fv heavy chain/light chain variable domain and exotoxin A fusion protein. If desired, the FLAG peptide can be cleaved off by enterokinase, preferably after affinity purification of the protein, yielding a fusion protein comprising the single-chain antibody Fv(FRP5) and exotoxin A.

Most preferred is a single-chain recombinant antibody wherein the heavy chain variable domain and the light chain variable domain are derived from a mouse monoclonal antibody directed to the extracellular domain of the growth factor receptor c-erbB-2, e.g. derived from the mouse monoclonal antibodies FRP5, FSP16, FWP51 or FSP77, particularly from the mouse monoclonal antibodies FRP5 or FWP51. Likewise preferred is a single-chain recombinant antibody wherein the spacer group linking the light chain and the heavy chain variable domains is a polypeptide comprising about 15 amino acids selected from glycine and serine, in particular wherein the spacer group is the 15 amino acid polypeptide consisting of three repetitive subunits of Gly-Gly-Glv-Glv-Ser.

Especially preferred is a single-chain antibody comprising the heavy chain variable domain of a mouse monoclonal antibody selected from the group consisting of FRP5, FSP16, FWP51 and FSP77, the 15 amino acid spacer group consisting of three repetitive subunits of Gly-Gly-Gly-Gly-Ser, the light chain variable domain of a mouse monoclonal antibody selected from the group consisting of FRP5, FSP16, FWP51 and FSP77 and an enzyme, for example a phosphatase such as the alkaline phosphatase phoA, or an exotoxin such as Pseudomonas exotoxin, or a variant thereof.

Particularly preferred is the particular single-chain recombinant antibody designated Fv(FRP5)-phoA comprising a polypeptide of the amino acid sequence 2 to 690 of SEQ ID NO: 5.

Likewise preferred is a single-chain recombinant antibody comprising a peptide facilitating purification, a cleavage site and a particular single-chain recombinant antibody selected from the group consisting of Fv(FRP5)-ETA and Fv(FWP51)-ETA, in particular a single-chain recombinant antibody comprising a polypeptide selected from the group consisting of a polypeptide of the amino acid sequence -10 to 606 of SEQ. ID NO: 10 and of a polypeptide of the amino acid sequence -10 to 606 of SEQ. ID NO: 11, said protein being subjected to in vitro cleavage by enterokinase, if desired.

Particularly preferred is a single-chain recombinant antibody comprising a protein selected from the group consisting of a polypeptide of the amino acid sequence 2 to 606 of SEQ ID NO: 10 and a polypeptide of the amino acid sequence 2 to 606 of SEQ ID NO: 11.

The invention further concerns the mouse monoclonal antibodies directed to the extracellular domain of the growth factor receptor c-erbB-2 and designated FRP5, FSP16, FSP77, and FWP51, which are secreted by the hybridoma cell lines FRP5, FSP16, FSP77, and FWP51, respectively. Most preferred are the mouse monoclonal antibodies designated FRP5 and FWP51.

The invention further concerns a method of manufacture of the recombinant antibodies and of the mouse mondonal antibodies of the invention. The antibodies are prepared by processes that are known per se, characterized in that host calls or hybridoma cells as defined further below producing such antibodies are multiplied in vitro or in vivo and, when required, the obtained antibodies are isolated. For example, the recombinant antibodies of the invention can be prepared by recombinant DNA techniques comprising culturing a transformed host under conditions which allow expression thereof and isolation as aid antibodies.

More specifically, the present invention also relates to a process for the production of a protein of the invention selected from the group consisting of a heavy chain murine variable domain, a light chain murine variable domain, a heavy chain murine variable domain and a light chain murine variable domain, a single-chain recombinant antibody, a flusion protein, and a flusion protein optionally comprising a peptide facilitating purification, a cleavage stee and a peptide spacer comprising culturing a host, e.g. E. coli, which has been transformed with a hybrid vector comprising an expression cassette comprising a promoter and a DNA coding for said protein which DNA is controlled by said promoter, and isolatine said ortopian.

In particular, the present invention relates to a process for the production of a protein of the invention selected from the group consisting of a heavy chain murine variable domain, a light chain murine variable domain, a leavy chain murine variable domain, a lingue-chain recombinant antibody, and a fusion protein optionally comprising a peptide facilitating purification, a cleavage site and a peptide spacer comprising culturing a host, e.g. E. coil, which has been transformed with a hybrid vector comprising an expression cassette comprising a promoter operably linked to a first DNA sequence encoding a signal peptide linked in the proper reading frame to a second DNA sequence encoding said protein, and isolating sald protein.

Multiplication of hybridoma cells or mammalian host cells in <u>vitro</u> is carried out in suitable culture media, which are the customary standard culture media, for example Dubacco's Modified Eagle Medium (DMEM) or RPMI 1640 medium, optionally replenished by a mammalian serum, e.g. fetal calf serum, or trace elements and growth sustaining supplements, e.g. feeder cells secul as normal mouse pertioneal exudate cells, spleen cells, bone marrow macrophages, 2-aminosthanol, insulin, transferrin, low density lipoprotein, celes cald, or the like. Multiplication of host cells which are bacterial cells or yeast cells is likewise carried out in suitable culture media known in the art, for example for bacterial medium LyR-DCYM, MZYM, MZM, Terfifs Broth, SOB, SOC, 2 x YT, or M9 Milnimal Medium, and for yeast in medium YPD, YEPD, Minimal Medium, or Complete Minimal Dropout Medium.

In vitro production provides relatively pure antibody preparations and allows scale-up to give large amounts of the desired antibodies. Techniques for bacterial cell, yeast or mammalian cell cultivation are known in the art and include homogeneous suspension culture, e.g. in an airlift reactor or in a continuous stirrer reactor, or immobilized or entrapped cell culture, e.g. in hollow fibres, microcapsules, on agarose microbeads or ceramic cartridges.

Large quantities of the desired antibodies can also be obtained by multiplying mammalian cells in vivo. For this purpose, hybridoms cells producing the desired antibodies are injected into histocompatible mammals to take growth of antibody-producing tumors. Optionally, the animals are primed with a hydroczarbon, especially mineral cills such as pristane (tetramethy-pentadecane), prior to the injection. After one to three weeks, the antibodies are isolated from the body fluids of those mammals. For example, hybridoma cells obtained by fusion of suitable myeloma cells with antibody-producing spleen cells from Bablc mice, or transfected cells derived from hybridoma cell line 59/20 that produce the desired antibodies are injected intrapertioneally into Bablc mice optionally pre-treated with pristane, and, after one to two weeks, sacitic fluid is stank from the animals.

The cell culture supernatants are screened for the desired antibodies, preferentially by immunofluorescent staining of cells expressing c-erbB-2, by immunoblotting, by an enzyme immunoassay, e.g. a sandwich assay or a dot-assay, or a radicimmunoassay.

For isolation of the antibodies, the immunoglobulins in the culture supernatants or in the ascitic fluid may be concentrated, e.g. by precipitation with armonium sulphate, dialysis against hygroscopic material such as polyethylene glycol, filtration through selective membranes, or the like. If necessary and/or desired, the anti-bodies are purified by the customary chromatography methods, for example get filtration, ion-exchange chromatography, chromatography over DEAE-cellulace and/or firmuno-plaffinity chromatography over DEAE-cellulace and/or firmuno-plaffinity chromatography.

chromatography with c-erbB-2 protein or with Protein-A.

The invention further concerns hybridoma cells secreting the monoclonal antibodies of the invention, in particular the hybridoma cell lines FRP5, FSP16, FSP77, and FWP51 deposited under the Budapest Treaty on November 21, 1990 at the European Collection of Animal Cell Cultures (ECACC) in Porton Down, Salibury, UK, under the accession numbers 90112115, 90112116, 90112117, and 90112118, respectively. Most prefered is the hybridoma cell line designated FRP5, ECACC number 90112116 for the hybridoma cell line designated FWP51, ECACC number 90112118. The preferred hybridoma cells of the invention are genetically stable, secrete monoclonal antibodies of the invention of the desired specificity and can be activated from deep-frozen cultures by thawing and rectoning.

The invention also concerns a process for the preparation of a hybridoma cell line secreting monoclonal antibodies directed by the extracellular domain of the growth factor receptor c-ehB-2, characterized in that a suitable mammal, for example a Balbic mouse, is immunized with purified c-erbB-2 protein, an antigenic carrier containing purified c-erbB-2 or with cells bearing growth factor receptor c-erbB-2, antibody-producing cells or the immunized mammal are tused with cells of a suitable mysionna cell line, the hybrid cells obtained in the fusion are cioned, and cell clones secreting the desired antibodies are selected. For example epicen cells of Balbic mice immunized with cells bearing c-erbB-2 are fused with cells of the myeloma cell line PAI or the myeloma cell line is paid to the contained hybrid cells are screened for secretion of the desired antibodies, and positive hybridoma cells are cloned.

Preferred is a process for the preparation of a hybriodoma cell line, characterized in that Balbic mice are immunized by injecting autocutaneously and/or intraperitoneally between 107 and 108 cells of the human breast tumor cell line SKBR3 containing a suitable adjuvant several times, e.g., four to six times, over several months, e.g. between two and four months, and spicen cells from the immunized mice are taken two to four days after the last injection and fused with cells of the mygloran cell line PAI in the presence of a fusion promoter, preferably polyethydene glycol. Preferably the myeloma cells are fused with a three- to twentyfold excess of spleen cells from the immunized mice in a solution containing about 30 % to about 50 % polyethylene glycol of a molecular weight around 4000. After the fusion the cells are expanded in suitable culture media as described hereinbefore, supplemented with a selection medium, for example HAT medium, at regular intervals in order to prevent normal myeloma cells from overgrowing the desired hybriddoma cells.

The invention also concerns recombinant DNAs comprising an insert coding for a heavy chain murine variable domain and/or for a light chain murine variable domain of antibodies directed to the extracellular domain of the growth factor receptor c-erbB-2 as described hereinbetore. By definition such DNAs comprise coding single stranded DNAs, double stranded DNAs consisting of said coding DNAs and of complementary DNAs thereto, or these complementary (engle stranded DNAs double stranded DNAs double stranded DNAs thereto, or these complementary (engle stranded DNAs thereto).

Furthermore, DNA encoding a heavy chain murine variable domain and/or for a light chain murine variable domain of antibodies directed to the extracellular domain of the growth factor receptor c-erbB-2 can be enzymatically or chemically synthezised DNA having the authentic DNA sequence coding for a heavy chain murine variable domain and/or for the light chain murine variable domain, or a mutant therof. A mutant of the authentic DNA is a DNA encoding a heavy chain murine variable domain and/or a light chain murine variable domain or the above-mentioned artibodies in which one or more daried set elight chain murine variable domain and/or set of the heavy chain murine variable domain or the artibody. Such a mutant DNA is also ne or more other armino acids. Preferably said modification(s) are replaced by other nucleotides with the new codons coding for the same armino acid(s). Such a mutant sequence is also a degenerated sequence. Degenerated sequences are degenerated within the meaning of the genetic code in that an unlimited number of nucleotides are replaced by other nucleotides without resulting in a change of the amino acid sequence originally encoded. Such degenerated sequences may be useful due to their different restriction sites and/or frequency of particular codons which are preferred by the specific host, particularly E. coll, to obtain an optimal expression of the heavy chain murine variable domain.

The term mutant is intended to include a DNA mutant obtained by in vitro mutagenesis of the authentic DNA according to methods known in the art.

The invention relates to a recombinant DNA comprising an insert coding for a heavy chain murine variable domain of a monoclonal antibody selected from the group consisting of the antibodies FRP5, FSP16, FSP77 and FWP51, or coding for an amino acid sequence homologous to said heavy chain variable domain.

In particular, the invention concerns a recombinant DNA comprising an insert coding for a heavy chain murine variable domain, which originates from genomic DNA or mRNA of the hybridoma cell lines RPP5, FSP16, FSP17 or FWP51, or which is hornologous to genomic DNA of said cell lines and codes for an amino acid sequence hornologous to the heavy chain variable domain of monodonal antibodies FRP5, FSP16, FSP17 or FWP51. Especially verferred is a recombinant DNA comorbing an insert coding for a heavy chain murine

variable domain, which originates from genomic DNA or mRNA of the hybridoma cell line FRP5, or which is homologous to genomic DNA of said cell line and codes for an amino add sequence homologous to the heavy chain variable domain of monoclonal antibody FRP5, or a recombinant DNA comprising an insert coding for a heavy chain murine variable domain, which originates from genomic DNA or mRNA of the hybridoma cell line FWP51, or which is homologous to genomic DNA of said cell line and codes for an amino acid sequence homologous to the heavy chain variable domain of monoclonal suntibody FWP51.

Preferred is a recombinant DNA comprising an insert odding for the polypeptide of formula I, wherein FR₁, R₂, R₃, R₄, CDR₆, CDR₈, and CDR₃, have the meanings as mentioned hereinbefore, optionally further containing introns. Expecially preferred is a recombinant DNA coding for the polypeptide of formula I comprising inserts coding for murine or human framework regions FR₁, R₃, R₅, R₅, and FR₆, and insert socing for complementarity determining regions of the DNA sequence 99 to 113 (CDR₁₀), the DNA sequence 156 to 206 (CDR₃₀), and the DNA sequence 93 to 332 (CDR₃₀) of SEG ID NO.4 or coding for complementarity determining regions of the DNA sequence 93 to 335 (CDR₃₀) of SEG ID NO.8. Most preferred is a DNA comprising an insert of the DNA sequence 9 to 365 of SEG ID NO.4 wherein optionally one or more, e.g. 1 to 10, nucleotides are replaced by other nucleotides, in particular a DNA comprising an insert of the DNA sequence 9 to 386 of SEG ID NO.4. Likewise preferred is a DNA comprising an insert of the DNA sequence 9 to 386 of SEG ID NO.8. Wherein optionally one or more, e.g. 1 to 10, nucleotides are replaced by other nucleotides, in particular a DNA comprising an insert of the DNA sequence 9 to 386 of SEG ID NO.8. Wherein optionally one or more, e.g. 1 to 10, nucleotides are replaced by other nucleotides, in particular a DNA comprising an insert of the DNA sequence 9 to 386 of SEG ID NO.8. Wherein optionally one or more, e.g. 1 to 10, nucleotides are replaced by other nucleotides, in particular a DNA comprising an insert of the DNA sequence 9 to 386 of SEG ID NO.8.

In a DNA wherein nucleotides of the sequence given in SEQ ID NO.4, or in a DNA wherein nucleotides of the sequence given in SEQ ID NO.8, are replaced by other nucleotides, such replacement is preferred when it does not after the amino acid sequence of the complementarity determining regions (CDRs) coded for. This means that such replacement of nucleotides may occur in the inserts coding for the framework regions (FRs) or in a position where it does not alter the amino acid coded for the to the degeneracy of the triptic codons.

Likewise the invention relates to a recombinant DNA comprising an insert coding for a light chain murine variable domain of a monoclonal antibody selected from the group consisting of the antibodies FRP5, FSP16, FSP77 and FWP51, or coding for an amino aold sequence homologous to said light chain variable domain.

More specifically, the invention concerns a recombinant DNA comprising an insert coding for a light chain untine variable domain, which originates from genomic DNA or mRNA of the hybridoma cell lines FRPS, FSP16, FSP77 or FWPS1, or which is homologous to genomic DNA of said cell lines and codes for an amino acid sequence homologous to the light chain variable domain of monoclonal antiblodies FRPS, FSP77 or FWPS1. Particularly preferred is a recombinant DNA comprising an insert coding for a light chain murine variable domain, which originates from genomic DNA or mRNA of the hybridoma cell line FRPS, or which is homologous to genomic DNA or Said cell line and codes for an amino acid sequence homologous to the light chain variable domain of monoclonal antibody FRPS, or a recombinant DNA comprising an insert coding for a light chain murine variable domain, which originates from genomic DNA or mRNA of the hybridoma cell line FWPS1, or which is homologous to genomic DNA or mRNA of the hybridoma cell line FWPS1, or which is homologous to genomic DNA or mRNA of the hybridoma cell line FWPS1, or which is homologous to genomic DNA or mRNA of the hybridoma cell line FWPS1, or which is homologous to genomic DNA or mRNA of the hybridoma cell line FWPS1, or which is homologous to genomic DNA or mRNA of the hybridoma cell line FWPS1, or which is homologous to genomic DNA or mRNA of the hybridoma cell line sequence homologous to the light chain variable domain of monoclonal antibout FWPS1.

Preferred is a recombinant DNA comprising an insert coding for the polypeptide of formula II, wherein FR₆, FR₇, FR₆, CDR₁₁, CDR₂₁, and CDR₃₁, have the meanings as mentioned hereinheitore, optionally further containing introns. Especially preferred is a recombinant DNA coding for the polypeptide of formula II comprising inserts coding for murine or human framework regions FR₆, FR₆, FR, and FR₆ and inserts coding for complementarity determining regions of the DNA sequence 480 to 512 (CDR₁₁), the DNA sequence 551 to 578 (CDR₂₂), and the DNA sequence 481 to 515 (CDR₃₁) of SEQ ID NO:4, or coding for complementarity determining regions of the DNA sequence 483 to 515 (CDR₃₁), the DNA sequence 561 to 581 (CDR₂₂), and the DNA sequence 675 to 701 (CDR₃₁) of SEQ ID NO:4.

Most preferred is a DNA comprising an insert of the DNA sequence 411 to 728 of SEQ ID NO.4, wherein optionally one or more, e.g., 1 to 10, nucleotides are replaced by other nucleotides, in particular a DNA comprising an insert of the DNA sequence 411 to 728 of SEQ ID NO.4. Likewise preferred is a DNA comprising an insert of the DNA sequence 414 to 728 of SEQ ID NO.2, wherein optionally one or more, e.g., 1 to 10, nucleotides are replaced by other nucleotides, in particular a DNA comprising an insert of the DNA sequence 414 to 728 of SEQ ID NO.3, or the DNA sequence 414 to 728 of SEQ ID NO.3. In a DNA wherein nucleotides of the sequence given in SEQ ID NO.4, or in a DNA wherein nucleotides of the sequence given in SEQ ID NO.3, are replaced by other nucleotides, such replacement is preferred when it does not alter the amino acid sequence of the complementarity determining regions (CDRs) coded for, as is described above for DNA coding for the heavy chain variable domain.

For the assembly of complete tetrameric immunoglobulin molecules and the expression of chimeric antibodies, the recombinant DNA inserts coding for heavy and light chain variable domains are fused with the corresponding DNAs coding for heavy and light chain constant domains, the transferred into appropriate

cells, for example after incorporation into hybrid vectors.

The invention therefore also concerns recombinant DNAs comprising an insert coding for a heavy chain murine variable domain of an antibody directed to the extracellular domain of c-erb8-2 fused to a human constant domain y, for example y1, y2, y3 or y4, preferably y1 or y4. Likewise the invention concerns recombinant DNAs comprising an insert coding for a light chain murine variable domain of an antibody directed to the extracellular domain of c-erb8-2 fused to a human constant domain to x7. preferably x.

In another embodiment the invention pertains to recombinant DNAs coding for a recombinant DNA wherein the heavy chain variable domain and the light chain variable domain are linked by way of a DNA insert coding for a spacer group, optionally comprising a signal sequence facilitating the processing of the amtibody in the host cell and/or a DNA coding for a peptide facilitating the purification of the antibody and/or a DNA coding for a cleavage site and/or a DNA coding for a peptide spacer and/or a DNA coding for an effector molecule.

The DNA coding for an effector molecule is intended to be a DNA coding for the above-mentioned effector molecules, particularly a DNA coding for alkaline phosphatase or Pseudomonas exotoxin A. The DNA encoding such an effector molecule has the sequence of a naturally occurring enzyme or toxin encoding DNA, or a mutant therof, and can be prepared by methods well known in the art. A mutant of the naturally occurring DNA encoding e.g. alkaline phosphatase or Pseudomonas exotoxin A, or a variant thereof can be obtained s.g. analogously to the methods described above.

Most preferred is a DNA comprising an insert of the DNA sequence 23 to 814 of SEQ ID NO:5, of the DNA sequence 88 to 2155 of SEQ ID NO:5 or of the DNA sequence 23 to 2155 of SEQ ID NO:5, wherein optionally one or more, e.g. 1 to 10, nucleotides are replaced by other nucleotides, in particular a DNA comprising an insert of the DNA sequence 23 to 2155 of SEQ ID NO:5.

Equally preferred ia a DNA comprising an insert of the DNA sequence 1 to 1911 of SEQ ID NO: 10, of the DNA sequence 97 to 1911 of SEQ ID NO: 10, or of the DNA sequence 97 to 1911 of SEQ ID NO: 10, wherein optionally one or more, e.g., 1 to 10, nucleotides are replaced by other nucleotides, in particular a DNA comprising an insert of the DNA sequence 1 to 1911 of SEQ ID NO: 10, or a DNA comprising an insert of the DNA sequence 10 to 1911 of SEQ ID NO: 11, of the DNA sequence 64 to 1911 of SEQ ID NO: 11, or of the DNA sequence 57 to 1911 of SEQ ID NO: 11, wherein optionally one or more, e.g., 1 to 10, nucleotides are replaced by other nucleotides, in particular a DNA comprising an insert of the DNA sequence 1 to 1911 of SEQ ID NO: 11.

Furthermore the invention concerns a recombinent DNA which is a hybrid vector comprising an insert coding for the variable domain of a murine heavy chain as described hereinbefore and/or an insert coding for the variable domain of a murine light chain as described hereinbefore, an origin of replication or an autonomously replicating sequence, one or more dominant marker sequences and, optionally, expression control sequences, signal sequences and additional restriction sites.

In a first embodiment the hybrid vector according to the invention comprises an expression cassette comprising a promoter and a DNA coding for a protein of the invention selected from the group consisting of a heavy chain murine variable domain, a light chain murine variable domain, a heavy chain murine variable domain and a light chain murine variable domain, a single-chain recombinant antibody, a fusion protein, and a fusion protein optionally comprising a peptide facilitating purification, a deavage site and a peptide spacer, which DNA is controlled by said promoter, and isolating said protein.

In a second embodiment, the hybrid vector according to the invention comprises an expression cassette comprising a promoter operably linked to a first DNA sequence encoding a signal peptide linked in the proper creating frame to a second DNA sequence encoding a protein of the invention selected from the group consisting of a heavy chain murine variable domain, a light chain murine variable domain, a heavy chain murine variable domain and a light chain murine variable domain and a light chain murine variable domain as well and a peolide spacer.

Vectors typically perform two functions in collaboration with competible host cells. One function is to facilitate the doring of the nucleic acid that encodes the immunoglobulin variable domains, i.e. to produce usable quantities of the nucleic acid (cloning vectors). The other function is to provide for replication and expression of the recombinant gene constructs in a suitable host, either by maintenance as an extrachronosomal element or by integration into the host chromosome (expression vectors). A cloning vector comprises the recombinant gene constructs as described above, an origin of replication or an autonomously replicating sequence, dominant marker sequences and optionally, signal sequences and additional restriction sites. An expression vector additionally comprises expression control sequences essential for the transcription and translation of the recombinant cenes.

An origin of replication or an autonomously replicating sequence is provided either by construction of the vector to include an exogeneous origin such as derived from Similan virus 40 (SV 40) or another viral source, or by the host cell chromosomal mechanisms.

The markers allow for selection of host cells which contain the vector. Selection markers include genes which confer resistance to heavy metals such as copper or to antibiotics such as geneticin (G-419) or typromy-cin, or genes which complement a genetic lession of the host cell such as the absence of thymidin kinase, hypoxantiline phosphory transferase, dhydrodiate reductase or the like.

Signal sequences may be, for example, presequences or secretory leaders directing the secretion of the recombinant antibody, splice signals, or the like. Examples for signal sequences directing the secretion of the recombinant antibody are sequences derived from the ompA gene, the pelB (pectate lyase) gene or the phoA gene.

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As expression control sequences, the vector DNA comprises a promoter, sequences necessary for the initiation and termination of transcription and for stabilizing the mRNA and, optionally, enhancers and further regulatory sequences.

A wide variety of promoting sequences may be employed, depending on the nature of the host cell. Promoters that are storing and at the same time well regulated are the most useful. Sequences for the initiation of translation are for example Shine-Dalgamo sequences. Sequences necessary for the initiation and termination of transcription and for stabilizing the mRNA are commonly available from the noncoding 5'-regions and 5'-regions, respectively, of viral or eukaryotic cDNAs, e.g., from the expression host. Enhancers are transcription-stimulating DNA sequences of viral origin, e.g. derived from Simian virus, polyoma virus, bovine papilloma virus or Moloney sarcoma virus, or of senomic, sessicially murine, origin.

The various DNA segments of the vector DNA are operationally linked, i.e. they are contiguous and placed into a functional relationship with each other.

Examples of vectors which are suitable for replication and expression in an <u>E. coli</u> strain are bacteriophages, for example derivatives of 1.5 bacteriophages, or plasmids, such as, in particular, the plasmid CollE1 and its derivatives, for example MB9, pSF2124, pBR317 or pBR322 and plasmids derived from pBR322, what as pUC9, pUCK0, pHR1148 and pLc24. Suitable vectors contain a complete replicon, a marker gene, recognition sequences for restriction endonucleases, so that the foreign DNA and, if appropriate, the expression control sequence can be inserted at these sites, and optionally signal sequences and enhances.

Microbial promoters are, for example, the strong leftward promoter P_c of bacteriophage. A which is controlled by a temperature sensitive repressor. Also suitable are <u>E_c coli</u> promoters such as the lac (lactose) promoter regulated by the lac repressor and induced by isoproply-B-D-thlogalactoside, the trp (tryptophan) promoter regulated by the propressor and induced e.g. by tryptophan starvation, and the tac (hybrid trp-lac promoter) regulated by the lac repressor.

Vectors which are suitable for replication and expression in yeast contain a yeast replication start and a selective genetic marker for yeast. One group of such vectors includes so-called are sequences (autonomous replication sequences) as origin of replication. These vectors are retained extrachromosomally within the yeast cell after the transformation and are replicated autonomously. Furthermore, vectors which contain all or port of the 2µ (2 mixtory) plasmid DNA from Saccharomyces cerevisiae can be used. Such vectors will get integrated by recombination into 2µ plasmids already existing within the cell, or replicate autonomously. 2µ sequences are particularly suitable when high transformation frequency and high copy numbers are to be achieved.

Expression control sequences which are suitable for expression in yeast are, for example, those of highly expressed yeast genes. Thus, the promoters for the TIRP1 gene, the ADHI or ADHII gene, acid phosphatase (PHO3 or PHO5) gene, isocytochrome gene or a promoter involved with the glycdytic pathway, such as the promoter of the enclase, glycera/dehyde3-phosphate kinase (PGK), hexokinase, pyruvate decarboxylase, phosphoffuctokinase, glucose-6-phosphate isomerase. 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglycose isomerase and glucokinase genes, can be used.

Vectors suitable for replication and expression in mammalian cells are preferably provided with promoting sequences derived from DNA of viral origin, e.g. from Simian virus 40 (SV40), Rous sarcoma virus (RSV).

adenovirus 2, bovine papilloma virus (BPV), papovavirus BK mutant (BKV), or mouse or human cytomegalovirus (CMV), Alternatively, the vectors may comprise promoters from mammalian expression products, such as actin, collagen, myosin etc., or the native promoter and control sequences which are normally associated with the desired gene sequence, i.e. the immunoglobulin H-chain or L-chain promoter.

Preferred vectors are suitable for both procaryotic and eucaryotic hosts and are based on viral replication systems. Particularly preferred are vectors comprising Simian virus promoters, e.g. pSVgpt or pSVneo, further comprising an enhancer, e.g. an enhancer normally associated with the immunoglobulin gene sequences, in particular the mouse Ig H- or L-chain enhancer.

The recombinant DNA coding for a recombinant antibody of the invention can be prepared, for example, by culturing a transformed host cell and optionally isolating the prepared DNA.

In particular, such DNA can be prepared by a method comprising

a) preparing murine DNA coding for the variable heavy and/or light chain domains of the antibody with the desired specificity, e.g. by isolating the DNA from the genome of a suitable hybridoma cell line and selecting the desired DNA using DNA probes, or by isolating mRNA from a suitable hybridoma cell line and preparing cDNA coding for the variable heavy and/or light chain domains of the antibody with the desired specificity using olionucleotide primers.

 b) preparing DNA coding for the desired signal sequence and/or preparing DNA coding for an effector molecule, e.g. by isolating the desired DNA(s) from a suitable source, e.g. from a genomic library or a cDNA library using DNA probes.

c) synthesizing DNA coding for the desired spacer group by chemical methods.

d) constructing recombinant genes encoding the recombinant antibodies by incorporating the DNA of step a) and, optionally, b) and/or c) into appropriate hybrid vectors,

e) transferring the obtained hybrid vectors into a recipient host cell or retrieving the DNA coding for the

recombinant genes and transferring the unlinked DNA into a recipient host cell, f) selecting and culturing the transformed host cell, and

g) optionally isolating the desired DNA.

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The DNA according to step a) of the process described above can be obtained by isolation of genomic DNA or by preparation of DNA from instalted mRNA. Genomic DNA from hybriddoms cells is isolated by methods known in the art which include steps for disruption of the cells, e.g. by lysis in presence of detergents like Trison™, extracting the DNA, e.g. by treatment with phenol and CHClylsoamyal alcohol, and precipitation of DNA The DNA is fragmented, conveniently by one or more restriction endounclesses, he resulting fragments are replicated on a suitable carrier, e.g., nitrocellulose membranes, and screened with a DNA probe for the presence of the DNA sequences coding for the polypeptide sequence by interest, in particular for the presence of the DNA sequences coding for the polypeptide sequence DNA fragments are found that contain inserts with heavy chain V, D and J regions and light chain V and J regions, respectively, together with a leader sequence and introns, if any. cDNA from hybridoma cells is likewise prepared by methods known in the art, e.g. by extacting total cellular RNA, solating mRNA by a suitable chromostographic method, e.g. chromatography on oligo(dT)-cellulose, synthesizing cDNA with a mixture of deoxynucleotide triphosphates and reverse transcriptase in the presence of oligonucleditie primers complementary to suitable regions in the murine immunoglobulin heavy and light chain constant domain genes, and isolating the CDNA. As a tool simplifying DNA isolation, the desired genomic DNA or CDNA may be amplified using observances chain reaction (PCR) isolation on the desired genomic DNA or CDNA may be amplified using observances and manufactures and control and control or con

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Genomic DNA or cDNA according to step b) of the process described above is isolated from suitable bactential or mammalian cells according to methods known in the art. Preferably, the methods as described under a) are used, substituting the corresponding source cells for the murine hybridoma cells and using DNA probes designed to hybridize with the desired signal sequences or the genes coding for the desired effector melocular in bacteria wherein separation of mRNA from total RNA is not possible with brigiQT1-celludose, cDNA is prepared from total RNA using corresponding oligonucleotide primers. The DNA isolation is simplified considerably by the PCR technology.

DNA according to step c) is prepared by conventional chemical and enzymatic methods, e.g. by chemical synthesis of oligonucleotides of between thirty and sixty bases with overlapping complementary sequences, hybridization of such oligonucleotides, and enzymatic ligation, optionally after filling-in of missing bases with suitable enzymes in the presence of the corresponding decovariated by this problem that is the property of t

The DNA probe for the mouse variable chain domains may be a synthetic DNA, a cDNA derived from mRNA coding for the desired immunoglobulin or a genomic DNA or DNA fragment of known nucleotide sequence. As

probes for the detection and/or amplification of the rearranged Ig gene loci of the variable domains of L-Hchains, DNA fragments of known nucleotide sequences of adjacent conserved variable or constant domains are selected which constitute the Ig loc of the L-H-chain in the mammal from which the DNA is derived, e.g. Balb/c mice. The DNA probe is synthesized by chemical methods or isolated from suitable tissue of an appropnate mammal, e.g. Balb/c mouse liver, and purified by standard methods. If required, the probe DNA is labelled, e.g. radioactively labelled by the well-known nick-translation technique, then hybridized with the DNA library in buffer and salt solutions containing adjuncts, e.g. calcium chelators, viscosity regulating compounds, proteins, non-sectific DNA and the like, at temperatures favorious elective hybridization.

Once a fragment has been identified which contains the desired DNA sequence, this fragment may be further manipulated to remove nonessential DNA, modified at one or both termini, and treated to remove all or a portion of intervening sequences, or the like.

The joining of the various DNA fragments in order to produce recombinant genes encoding the recombinant antibodies is performed in accordance with conventional techniques, for example, by blunt- or staggered-end ligation, restriction enzyme digestion to provide for appropriate cohesive termini, filling-in cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and ligation with appropriate ligases.

The transfer of the recombinant DNAs, e.g. the transfer of hybrid vectors, and the selection of transformed

Moreover, the invention relates to host cells transformed with the recombinant DNAs described above, namely host cells which are transformed with a DNA encoding the heavy chain and/or a DNA encoding the light chain of the desired recombinant antibody, in particular host cells transformed with a DNA encoding the preferred single-chain recombinant antibody.

More specifically, the invention concerns a host cell which has been transformed with a hybrid vector comprising an expression cassatte comprising a promoter and a DNA coding for a protein of the invention selected from the group consisting of a heavy chair murtine variable domain, a light chain murine variable domain, a heavy chair murine variable domain and a light chair murine variable domain, a single-chair recombinant antibody, a fusion protein, and a fusion protein further comprising a peptide facilitating purification, a cleavage site and a peptide spacer which DNA is controlled by said promoter.

Furthermore, the invention pertains to a host cell which has been transformed with a hybrid vector comprising an expression cassette comprising a promoter operably linked to a first DNA sequence encoding a signal peptide linked in the proper reading frame to a second DNA sequence encoding a protein of the invention setected from the group consisting of a heavy chair murine variable domain, a light chair murine variable domain, a a heavy chair murine variable domain and a light chair murine variable domain, a single-chair recombinant antibody, a fusion protein, and a fusion protein further comprising a peptide facilitating purification, a cleavage site and a peptide spacer.

In particular, the present invention relates to a process for the production of a protein of the invention selected from the group consisting of a heavy chain murine variable domain, a light chain murine variable domain, a heavy chain murine variable domain, a single-chain recombinant antibody, a fusion protein, and a fusion protein further comprising a peptide facilitating purification, a cleavage site and a peptide spacer comprising culturing a host, e.g. E. coll, which has been transformed with a hybrid vector comprising an expression cassette comprising a promoter operably linked to a first DNA sequence encoding a signal peptide linked in the proper reading frame to a second DNA sequence encoding said protein, and isolating easil protein.

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The host cells of the present invention have to be capable of culture in vitro. Suitable host cells are of procaryotic or of eucaryotic origin and are, for example, bacterial cells, e.g. <u>E. coll</u>, yeasts, e.g. <u>Seacharomyces cerevisiae</u>, or mammalian cells. For the preparation of functional chimeric human/mouse anbitodies the host cells have to be of higher eucaryotic origin to provide a suitable environment for the production of active antibodies, since the biosynthesis of functional tetrameric antibody molecules requires correct nascent polypeptide chain folding, obcosylation, and assembly.

The above mentioned strains of E. coli, in particular E. coli CC118, are preferred as hosts.

The invention also concerns processes for the preparation of transformed host cells wherein suitable recipient host cells as described hereinbefore are transformed with a hybrid vector according to the invention, and the transformed cells are selected.

Transformation of microorganisms is carried out as described in the literature, for example for <u>S. cerevisiae</u> (A.Hinnen etal., Proc. Natl. Acad. Sci. USA 75: 1929, 1978), for <u>B. subtilis</u> (Anagnostopoulos et al., J. Bacteriol. 81: 741, 1961), and for E. coil (M. Mandel et al., J. Mol. Biol. 53: 159, 1970).

Accordingly, the transformation procedure of <u>E. coli</u> cells includes, for example, Ca²⁺ pretreatment of the cells so as to allow DNA uptake, and incubation with the hybrid vector. The subsequent selection of the transformed cells can be achieved, for example, by transferring the cells to a selective growth medium which allows separation of the transformed cells from the parent cells dependent on the nature of the marker sequence of the vector DNA. Preferably, a growth medium is used which does not allow growth or cells which do not contain the vector. The transformation of yeast comprises, for example, steps of enzymatic removal of the yeast cell wall by means of glucosidases, treatment of the obtained spheroplasts with the vector in the presence of polyethylene glycol and Ca²⁺ lons, and regeneration of the cell wall by embedding the spheroplasts into agar. Preferably, the regeneration agar is prepared in a way to allow regeneration and selection of the transformed cells as described above at the same time.

Transformation of cells of higher eucaryotic origin, such as mammalian cell lines, is preferably achieved by transfection. Transfection is carried out by conventional techniques, such as calcium phosphate precipitation, micronijection, protoplast fusion, electroporation, i.e. introduction of DNA by a short electrical pulse which translently increases the permeability of the cell membrane, or in the presence of helperocompounds such as diethylaminorthyldextran, dimethyl sulfcode, glycerol or polyethylene glycol, and the like. After the transfection procedure, transfected cells are identified and selected, for example, by cuttivation in a selective medium chosen depending on the nature of the selection marker, for example standard culture media such as Dubecco's modified Eagle medium (DMEM), minimum essential medium, RPMI 1840 medium and the like, containing e.q. the corresponding antibiotic.

The host cells are transformed with the recombinant L-chain gene construct alone, with the recombinant L-chain gene construct alone, with both, either sequentially or simultaneously, or by using a vector construct comprising both the L-chain and H-chain genes, for example a recombinant single-chain artibody gene construct as indicated hereinbefore.

Preferred are host cells transformed with a recombinant single-chain antibody gene construct comprising DNA coding for the heavy chain variable domain of an anti-e-orb8-2 antibody, DNA coding for a specer group, DNA coding for the light chain variable domain of an anti-o-orb8-2 antibody and DNA coding for an effector molecule, in particular transfected with the preferred recombinant single-chain antibody gene construct as indicated hereinbefore. Further examples of host cells of the invention are cells transfected with similar recombinant plasmids which contain alternative orientations of the H- and L-chain gene constructs, and those incorporating additional DNA elements to facilitate high levels of expression of the recombinant antibodies.

The host cells of the invention are genetically stable, secrete recombinant antibodies of the invention of constant specificity and can be activated from deep-frozen cultures by thawing and recioning.

The transformed host cells are cultured by methods known in the art in a liquid medium containing assimilable sources of carbon, e.g. carbohydrates such as glucose or locatose, nitrogen, e.g. armino acids, peptides, proteins or their degradation products such as peptones, ammonitum saits or the like, and inorganic saits, e.g., surfaces, phosphates and/or carbonates of socialim, potassium, angenesium and calcium. The medium further-more contains, for example, growth-promoting substances, such as trace elements, for example iron, zinc, mananese and the like.

The medium is preferably so chosen as to exert a selection pressure and prevent the growth of cells which have not been transformed or have lost the hybrid vector. Thus, for example, an antibiotic is added to the medium if the hybrid vector contains an antibiotic resistance gene as marker. If, for instance, a host cell is used which is auxctrophic in an essential amino acid whereas the hybrid vector contains a gene coding for an enzyme which complements the host defect, a minimal medium deficient of said amino acid is used to culture the transformed cells.

Cells of higher eucaryotic origin such as mammalian cells are grown under tissue culture conditions using commercially available media, for example Dubbecoo's modified Eagle medium (DMEM), minimum essential medium, RPMI 1840 medium and the like as mentioned above, optionally supplemented with growth-promoting substances and/or mammalian sera. Techniques for cell cultivation under tissue culture condition are well known in the art and include homogeneous suspension culture, e.g., in an artifit reactor or in a continuous stirer reactor, or immobilized or entrapped cell culture, e.g. in hollow fibres, microcapsules, on agarose microbeads, porque slasse beds, ceramic cartifides os or other microcarriers.

Culturing is effected by processes which are known in the art. The culture conditions, such as temperature, pH value of the medium and fermentation time, are chosen so that a maximum titer of the polypeptide or derivative of the invention is obtained. Thus, an E_culty resets that in preferably cultured under serobic conditions by submerged culture with shaking or stirring at a temperature of about 20°C to 40°C, preferably at about 30°C, and a pH value of 4 to 8, preferably of about pH 7, for about 4 to 30 hours, preferably until maximum yields of the polypeptide or derivative of the invention are reached.

When the cell density has reached a sufficient value, the culture is interrupted and the polypeptide or derivative can be isolated. If the hybrid vector contains a suitable secretion signal sequence, the polypeptide or derivative is excreted by the transformed cell directly into the culture medium. Otherwise, the cells have to be destroyed, for example by treatment with a detergent such as SDS, NP-40 "In Triton" or deoxycholic acid, lysed with ysozyme or a similarly aciding nexyme, or disrupted by an osmotic shock or ultra-sound. Break-up of the cells will also be required if the signal sequence directs the secretion of the desired protein into the cell peripleam. If yeast is used as a host microorganism, the cell wall may be removed by enzymatic digestion with a glucosidase. Alternatively or additionally, mechanical forces, such as shearing forces (e.g. French press, Dyno mill and the like) or additionally and achieved and the like or additionally and the seads or aluminium coide, or alternating freezing, for example in liquid infrocen, and then, for example at 30°C to 40°C, as well as utilization used to break the cells.

The cell supernatant or the solution obtained after centrifugation of the mixture obtained after breaking the cells, which contains proteins, nucleic acids and other cell constituents, is enriched in proteins, including the polypeptides of the invention, in a manner which is known per gas. Thus, for example, most of the non-protein constituents are removed by polyethyleneimine treatment and the proteins including the polypeptides and derivatives of the invention are precipitated, for example, by saturation of the solution with ammonium suffate or with other saits. Otherwise, the cell supernatant or lysate is directly pre-purified by filtering through suitable membranes and/or with chromatographic methods, for example affinity chromatography.

The recombinant antibodies and the monoclonal antibodies according to the invention can be used for the qualitative and quantitative determination of the extracellular domain of the growth factor receptor c-erb8-2. This is especially useful for the monitoring of tumor progression, for the decision whether a tumor is amenable to treatment with the recombinant or monoclonal antibodies of the invention, and for monitoring the treatment of tumor with chemotherapy. Tumors considered are those over-expressing c-erb8-2, for example breast and ovarian tumors.

In general, the monoclonal and the recombinant antibodies according to the invention can be used in any of the known immunoassays which rely on the binding interaction between the antibodies and the antigen, i.e. the extracellular domain of the c-erb8-2 protein. Examples of such assays are radio-, enzyme, fluorescence, chemiluminescence, immunoprecipitation, latex agglutination, and hemagglutination immunoassays, and, in particular, immunostaining methods.

The antibodies according to the invention can be used as such or in the form of enzyme-conjugated derivatives in an enzyme immunoassay. Any of the known modifications of an enzyme immunoassay can be used, for example soluble phase (homogeneous) enzyme immunoassay, solid phase (heterogeneous) enzyme immunoassay, single enzyme immunoassay, single enzyme immunoassay or double (sandwich) enzyme immunoassay with direct or indirect (competitive) determination of the c-ethPs2 protein.

An example of such an enzyme immunoassay is a sandwich enzyme immunoassay in which a suitable carrier, for example the plastic surface of a microtiter plate or of a test tube, e.g. of polysylvene, polypropylene or polyvinyhidroide, gleas or plastic beads, filter paper, dextran eta. cellulose acetate or nitrocellulose sheets, magnetic particles or the like, is coated with a monoclonal antibody of the invention by simple adsorption or optionally after activation of the carrier, for example with glutrardehyde or cyanopen bromice. Then test solutions containing the soluble c-erbB-2 protein and finally single-chain recombinant antibodies of the invention comprising a detectable enzyme, e.g. alkaline phosphatase, are added. The amount of the soluble c-erbB-2 protein in the test solution is directly proportional to the amount of bound recombinant antibody and is determined by adding an enzyme substrate solution. The enzyme substrate reaction results, for example, in a color change which can be observed by eye or with optical measuring devices.

The antibodies according to the invention can be used as such or in the form of radioactively labelled derivatives in a radioimmunoassay (RIA). As described above for enzyme immunoassays, any of the known modffications of a radioimmunoassay can be used.

The tests are carried out in an analogous manner to the enzyme immunoassays described above using a radioactive label, e.g. 1²⁸, Instand of an enzyme label. The amount of immune complex formed which corresponds to the amount of cerbB-2 protein present in the test solutions is determined by measuring the radioactivity of the immune complex.

For immunostaining cryosections of cryopreserved biopsy material or paraffin embedded tissue sections are treated with a solution containing a recombinant antibody of the invention comprising a detectable enzyme.

Bound recombinant antibody is detected by treatment with a suitable enzyme substrate, preferably an enzyme substrate which leads to a solid deposit (stain) at the site of the recombinant antibody of the invention. In place of recombinant antibodies comprising an enzyme, a recombinant antibody comprising streptavidin and a solution of a biotin-enzyme-conjugate may be used, which leads to higher enzyme concentration at the site of manibody and mence increased sensitivity of the immunostaining method. The solid deposit of the enzyme substrate is detected by inspection with a microscope, for example with a fluorescence microscope, or by scanning the optical density at the wavelength of the stain.

The use according to the invention of recombinant and/or monoclonal antibodies as described hereinbefore for the determination of o-erb8-2 protein also includes other immunossasya known per se, for example immunofluorescence assays, latex agolutination with antibody-coated or antibody-coated optical fibre and other direct-acting immunosensors which convert the binding event into an electrical or optical signal, or the like.

The invention also concerns test kits for the qualitative and quantitative determination of c-erb8-2 protein comprising recombinant antibodies of the invention and/or monodonal antibodies of the invention and, optionally, adjuncts.

Test kits according to the invention for an enzyme immunoassay contain, for example, a suitable carrier, optionally freeze-dried solutions of a monodonal antibody, optionally freeze-dried or concentrated solutions of a recombinant antibody comprising an enzyme or streptavidin, solutions of an enzyme-biotin conjugate if a recombinant antibody comprising streptavidin is used, enzyme substrate in solid or dissolved form, standard solutions of e-orth-2-protein, buffer solutions, and, optionally, optypeptides or detergents for preventing non-specific adsorption and aggregate formation, pipettes, reaction vessels, calibration curves, instruction manuals and the like.

Test kits according to the invention for immunostaining contain, for example, optionally freeze-dried or concentrated solutions of a recombinant antibody comprising an enzyme or streptavidin, solutions of an enzymebiotin conjugate if a recombinant antibody comprising streptavidin is used, enzyme substrate in solid or dissolved form, buffer solutions, and, optionally, pipettes, reaction vessels, calibration curves, instruction manules and the like

The recombinant and monoclonal antibodies of the invention can be used for the qualitative and quantitative determination of c-erbB-2 protein. Due to the fact that the growth factor receptor c-erbB-2 is overexpressed in certain tumor types, for example breast and ovarian tumors, the antibodies are particularly well suited for detection and monitoring of the mentioned tumors. In addition, radiolabelled derivatives of the antibodies of the invention may be used for the invention calculation of tumors in a patient using radioscanning techniques. To that end, radiolabelled derivatives of antibodies of the invention are injected into the patient, and the patient scanned with a gamma imager at regular intervals. Cells over-expressing the growth factor receptor c-erbB-2 will take up more radioactive antibodies than other tissue and will be dearly recognized by the gamma imaging camera. Preferentially recombinant or monoclonal antibodies labelled with 191 or with term? care used for radioscanning in amounts of 3 to 8 µg representing 15 to 30 µg to presenting 15 to 30 µg to present 15 µg to pres

The antibodies of the invention can further be used for the isolation and purification of the c-erbB-2 protein from natural sources or from transformed host cells by immunoaffinity chromatography.

Furthermore, the monoclonal antibodies and the recombinant antibodies of the invention, in particular recombinant antibodies comprising an effector molecule, especially a toxin, in particular Pseudomonas exotoxin, are useful for the treatment of patients with tumors over-expressing the growth factor receptor c-erbB-2, for example breast or ovarian tumors. If it is desired, tumor therapy may comprise applying more than one, e.g. two different, antibodies of the invention, for example applying both FRP5 and FWP51. The recombinant antibodies comprising a phosphatase may be used in connection with a phosphorylated prodrug such as mitomycin phosphate or etoposide phosphate, thus enabling the conversion of the active drug to the prodrug at the site of the tumor.

The invention therefore also concerns pharmaceutical compositions for treating tumors over-expressing the growth factor receptor c-erbe2 comprising a therapeutically effective amount of a recombinant antibody or of a monoclonal antibody according to the invention and a pharmaceutically acceptable carrier. Preferred are pharmaceutical compositions for parenteral application. Compositions for intramuscular, subcutaneous or intravenous application are e.g. isolatonic aqueous solutions or suspensions, optionally prepared shortly before use from lyophilized or concentrated preparations. Suspensions in oil contain as oily component the vegetable, synthetic or semi-synthetic oils customary for injection purposes. The pharmaceutical compositions may be sterilized and contain adjuncts, e.g. for conserving, stabilizing, wetting, emulsifying or solublizing the ingredients, satis for the regulation of the comotic pressure, buffer and/or compounds regulating the viscosity, e.g. accidium carboxycellulose, cardoxymethylocallulose, sodium carboxycellulose, externa, polyrinylymyroli-

dine or gelatine.

The pharmaceutical compositions of the invention contain from approximately 0.01% to approximately 50% of active ingredients. They may be in dosage unit form, such as ready-to-use ampoules or vials, or also in lyophylized solid form.

In general, the therapeutically effective dose for mammals is between approximately 5 and 25 µg of a recombinant antibody of the invention or of a monoclonal antibody of the invention per kg body weight depending on the type of antibody, the status of the patient and the mode of application. The specific mode of administration and the appropriate dosage will be selected by the attending physician taking into account the particulars of the patient, the state of the disease, the type of tumor treated, and the like. The pharmaceutical compositions of the invention are prepared by methods known in the art, e.g. by conventional mixing, dissolving, confectioning or lyophilizing processes. Pharmaceutical compositions for injection are processed, filled into amoutes or visits, and seeled under seeptic conditions according to methods known in the art.

The invention particularly concerns the monodonal antibodies, the hybridoma cell lines, the recombinations single-chain antibodies, the coronbinant DNAs, the transformed host cells, and the methods for the preparation thereof as described in the Examples. The following examples illustrate the Invention but do not limit it to any extent.

Abbreviations

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0	ATP	adenosine triphosphate
	BSS	Earle's balanced salt solution
	BSA	bovine serum albumin
	DEAE	diethylaminoethyl
	DMEM	Dulbecco's modified Eagle's medium
5	dNTP	deoxynucleotide triphosphate
	DTT	dithiothreitol
	EDTA	disodium ethylenediaminetetraacetate
	EGF	epidermal growth factor
	EGTA	ethyleneglycol-bis-(β-aminoethyl ether)-N,N,N',N'-tetraacetic acid
0	FCS	fetal calf serum
	HAT medium	hypoxanthine, aminopterin and thymidine medium
	HEPES	N-2-hydroxyethylpiperazine-N'-2-ethanesulfonic acid
	HT medium	hypoxanthine and thymidine medium
	lg	immunoglobulin
5	IPTG	isopropyl-β-thiogalactoside
	MAb	monoclonal antibody
	PBS	phosphate-buffered saline
	PCR	polymerase chain reaction
	PMSF	phenylmethylsulfonyl fluoride
9	SDS-PAGE	sodium dodecyl sulfate-polyacrylamide gel electrophoresis
	Tris	Tris-(hydroxymethyl)-aminomethane
	U	unit
	V _L	light chain variable domain
	V _H	heavy chain variable domain
5	XP	5-bromo-4-chloro-3-indolyl phosphate p-toluidine salt

Examples

Example 1. Preparation of hybridoma cell lines FRP5, FSP16, FWP51 and FSP77

- 1.1 Source of antigen and immunization of Balb/c mice: The SKBR3 human breast tumor cell line (ATCC HITO) solds), isolated in 1970 from a pleural effusion of a breast cancer patient, expresses approximately 1 x 10⁸ molecules of the c-erbB-2 receptor protein per cell. 20 x 10⁸ SKBR3 cells in PBS are injected subctaneously and/or intra-pertioneally into Balb/c mice. The cells are mixed 111 (v/v) with complete Freund's adjuvant. The injections are repeated a total of five times over the period of approximately 3 months replacing Freund's incomplete adjuvant for complete adjuvant. The final injection of cells is given three days before the fusion.
- 1.2 Cell fusion: Immunized mice are sacrificed and their splenocytes fused according to conventional methods (Koehler & Milstein, Nature 256:495, 1976). Spleen cells are mixed at a 5:1 to 10:1 ratio with the fusion

partner, the mouse myeloma cell line PAI (Stoker et al., Research Disclosure #21713, 1982), in the presence of 41 % polyethylene glycol 4000 (Merck). Fused cells are plated at a density of 1 x 10⁹ cells per well in 24-well microtiter plates on peritoneal macrophages and fed 3 times per week with standard HAT selection medium for 2 weeks followed by 2 weeks of HT medium. When the growth of hybridoma cells becomes visible, the supernataths are screened as described in Example 1.3. Postike hybridomas are cloned and stored.

1.3 Antibody detection in hybridoma supernatants: Culture fluids of growing hybridomas are tested for the presence of anti-o-erbB-2 antibody using a protocol involving two steps, immunofluorescence and immunoprecipitation.

1.3.1 Immunofluoreacence. In the first step, hybridoma supernatants are tested for their immunofluoreacent staining of mouse cells expressing high levels of the human o-erb8-2 protein. To isolate these cells the HC11 mouses mammary epithelia cell line (Ball et al., EMBO J. 7: 2098, 1988) is transfected according to conventional, previously described methods (Graham & van der Eb, Virology 52: 456, 1973) with a plasmid expressing the human o-erb8-2 protein (Massuce et al., Jpn. Caneor Res. 80: 10, 1989) and with the plasmid pSV2nce (Southern & Berg, J. Mol. Appl. Genet. 1: 327, 1982) which encodes the gene for resistance to the drug G418. Transfected cells are selected a weeks in medium containing 200 µg/m G418 (Genetion, Gibco 8RL), Individual clones are selected and analyzed for expression of the human o-erb8-2 protein using conventional protein bloing techniques (Towin et al., Proc. Natl. Acad. Sol. USA 76: 4350, 1979). A clone expressing high levels of the human o-erb8-2 protein (clone R1#11) is selected and used in the immunofluorescent assay. Non-transfected HC11 cells serve as control cells.

The assay is done in the following manner. The cells (R1 #11 or HC11) are grown in RPMI medium containing 8 % heat inactivated FCS (Amimed), 10 ng/lm EGP (Inotech) and 5 µg/m1 insulin (Signay) for 1-2 days on fibronectin (Boehringer Mannheim) coated cover slips. Fibronectin coated cover slips are prepared and stored at room temperature and they are used routinely for screening. The coverslips are released in PBS containing calcium and magnesium and fixed by treatment for 10 min with 3.7 % formatidehyde (v/v in PBS). To reduce the non-specific binding the coverslips are incubated 20 min in PBS containing 3 % BSA (Sigma). The coverslips are washed in PBS and in water, then allowed to dry at room temperature. 20 - 30 µl of hyphridoma supermatants are added to circled areas on a coverslip which is incubated 1 - 2 h at room temperature in a humified atmosphere. The coverelips are then washed three times with PBS containing 0.05 % Tino-X100™ (Fluka) and incubated an additional hour with anti-mouse Ig, fluorescein-linked whole antibody from sheep (Amersham). After three washes with PBS and non wash with water the cells are screened for florescence using a fluorescence microscope and a water immersion lens. Those hybridoma supernatants which are positive are screened for florescence that the are positive are screened for florescence and a water immersion lens. Those hybridoma supernatants which are positive are screened for florest per described in Example 13.2.

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1.3.2 Immunoprecipitation and protein blotting analysis: The SKBR3 human breast tumor cells express approximately 1 x 106 molecules of the c-erbB-2 protein per cell. A cell lysate is prepared by extracting approximately 4 x 10⁶ cells in 1 ml of buffer containing 1 % Triton-X100™ (Fluka), 50 mM Tris-HCl, pH 7.5, 5 mM EGTA, 0.15 M NaCl, 1 mM PMSF (Boehringer Mannheim), 80 µg/ml aprotinin (Boehringer Mannheim), 50 μα/ml leupeptin (Boehringer Mannheim), and 4 μα/ml pepstatin (Boehringer Mannheim), 200 -500 μl supernatant of hybridomas which are positive in the immunofluorescence assay described in Example 1.3.1 are incubated with 100 µl of the SKBR3 extract (2.5 - 4.0 mg/ml). This amount of extract contains approximately 50 -100 ng of c-erbB-2 protein. The hybridoma supernatants and SKBR3 extract are incubated overnight on ice. then 1 ul of the IgG fraction of sheep anti-mouse Ig (ICN Immunobiologicals) is added. The complexes are collected by the addition of Protein-A Sepharose™ (Pharmacia), washed with TNET (140 mM NaCl, 50 mM Tris-HCl, pH 7.5, 5 mM EDTA, 1 % Triton X-100™) and water, boiled in sample buffer (80 mM Tris-HCl, pH 6.8, 0.2 % SDS, 10 % glycerol) and the supernatants loaded onto 8 % SDS-PAGE. The proteins are electrophoresed and blotted onto PVDF membranes (Millipore) using a technique originally described by Towbin et al. (Proc. Natl. Acad. Sci. USA 76: 4350, 1979) with some modifications. The proteins are transferred using a semi-dry blotter (G. Frobel, Model 1004.01) following the instructions of the manufacturer. The membranes are blocked in PBS containing 0.5 % gelatin (Merck) for 1 h at 37°C. The membranes are washed twice for 5 min at 37°C in PTG (PBS containing 0.02 % gelatin (Merck) and 0.25 % Triton-X100™ (Fluka)). The c-erbB-2 protein is detected by incubating the membrane 45 min at 37°C in PTG containing an antiserum which is raised against the carboxy terminal 13 amino acids of the c-erbB-2 protein (Gullick et al., Int. J. Cancer 40: 246, 1987, antiserum 21N). The membranes are washed 3 times for 5 min at 37°C in PTG. The membrane-bound 21N antiserum is detected by incubating the membrane in PTG containing 0.1 μC/ml ¹²⁵I-labeled protein-A (Amersham). The membranes are washed 4 times for 5 min at 37°C in PTG and exposed to X-ray film. The hybridomas whose supernatants are able to specifically immunoprecipitate the c-erbB-2 protein are grown for single cell cloning and further characterization described below.

Example 2. Characterization of c-erbB-2 specific MAbs

- 2.1 Hybridoma storage and processing: Hybridoma FRPS, FSP16, FWPS1 and FSP77 secreting anti-cerb2-2 MAb FRPS, FSP16, FWPS1 and FSP77, respectively, can be grown in culture, frozan at -80°C or in liquid nitrogen and recultivated. The cells are doned by the method of limiting diution and have been deposited with the European Collection of Animal Cell Lines in England. The hybridoma cell lines have the following access numbers: FRPS: 90112115, FSP18: 90112115, FSP
- 2.2 Isotyping of the MAbs: The isotype of the MAbs FRP5, FSP16, FWP51 and FSP77 is determined by ELISA analysis with rabbit antisera to mouse Ig classes and sub-classes (Biorad Mouse Type TMSub isotyping Kit¹⁴) as per manufacturer's suggested procedure. MAbs FRP5, FWP51, and FSP77 are of the IgG1 isotype, while FSP16 is of the IgG2b isotype. The light chains of all the MAbs are of the kappa type.
- 2.3 Flow cytometry. A FACS analysis using this c-erb8.2 specific MAbs is carried out as follows: SKBR3 ham breast tumor cells are typisalized, washed in FACS medium (BSS containing 10 µM socilum azide, 4 % FCS and 25 m M EDTA), and 1 x 10° cells are resuspended in 100 µl of FACS medium. Non-specific binding altes are oblocked by unloating the cells 10 min at room temperature with 5 µl of goat serum. The SKBR3 cells are collected by centrifugation, resuspended in 50 µl of a 1.2 ditution of the supernatart made in FACS medium and incubated 45 min on ice. The cells are washed with 4 mi FACS medium, collected by centrifugation, resuspended in 50 µl of FACS medium and incubated 45 min on ice. The cells are washed with 4 mi FACS medium are added, the cells are collected by centrifugation, resuspended in 50 µl of FACS medium and analyzed without fixation for their fluorescence in a Becton-Dickinson FACScan™. As a control, SKBR3 cells are incubated with a non-reacting IgG1 MAb (1288314.3). The FACS analysis shows that the SKBR3 cells the stead with MAb FRPS, FSP16, FMP51, and FSP77 have a higher fluorescence than cells treated with the control MAb. These results show that the MAbs bind to the extracellular domain of the c-erb8.2 protein.
- 2.4 Binding domain of certb-2 specific MAbs: MAbs FRP5 and FSP77 are covalently linked with ¹²⁹ (as carrier free solution ²³0dide, Amersham) to a specific activity of 1 µC/pu sing loodogen (1.3,4-6-tertachror-3a,6a-diphenylg/ycourli, Sigma) according to a standard protocol (Antibodiex A Laboratory Manual, Cod Spring Habor Laboratory, 1886, p. 330). Competition experiments are conducted by incubating SigR3 calls (0.5 1 x 10⁶ cells per 15 mm well, Nuncton ¹¹⁴ 4-well multidish) with 250 µl RIA buffer (120 mM NaCl, 50 mM HEPES, PH 7.8, 1 mM EDTA, 2 % BSA) containing labeled FRP5 or FSP17 and varying amounts of untable data MAs FRP6, FSP16, FWP51 and FSP17 for 2 h at 4°C. The cells are washed 5 times with the RIA buffer, solublized in 0.5 ml 1 % Trition X-100¹¹, 10 % glycerd, 20 mM HEPES, PH 7.4, for 30 min at room temperature and the bound radioactivity is measured in a gamma counter. The results show that MAbs FRP6 and FSP16 compete with each other for binding to SikR93 cells which suggests that these 2 MAbs bind to the same domain the c-erbS-2 protein. MAbs PKP61 and FSP17 neither compete with each other nor with FRP5 or FSP16 for binding to the cerbS-2 protein. In conclusion, the panel of 4 MAbs bind to 3 different domains of the extracellular portion of the c-erbS-2 membrane receptor tryosine kinses.

Example 3. Isolation of RNA from the hybridoma cell line FRP5

- 3.1 Growth of FRPS cells: FRPS hybridoma cells (1 x 109) are grown in suspension culture at 37°C in DMEM (Seromed) further containing 10 % FCS (Amimed), 1 mMs sodium pyruvate (Seromed), 2 mM glutamine (Seromed), 50 µM 2-mercaptoethand and 100 µg/ml of gentamyin (Seromed) in a brundlified atmosphere of air and 7.5 % CO₂ in 175 cm tissue culture flasks (Falcon 3028). The cells are harvested by centrifugation, washed once in PBS, flash frozen in liquid nitrogen and kept frozen as a pellet at -80°C in a clean, sterile plastic capped tube.
- 3.2 Extraction of total cellular RNA from FRPS cells: Total RNA is extracted using the acid quantifinium thioxyantat--penel-othordrom method described by Chomczynski & Sacchi (Anal. Blochen, 162: 156, 1987). Cell pollets of FRPS cells (1 x 10⁹) are thaveed directly in the tube in the presence of 10 ml of denaturing solution (4 M guantifinium thioxyantate (Fluka), 25 mM sodium citrate, pH 7.0, 0.5 % N-lauroy/sarcosine (Sigma), 0.1 M 2-mercaptoethanol). The solution is homogenized at room temperature. Sequentially, 1 ml of 2 M sodium acetate, pH 4, 10 ml of phenoi (water saturated) and 2 ml of chlordrom-isoamyl alcohol mixture (49:1) are added to the homogenate. The finial suspension is shaken vigorously for 10 sec and cooled on ice for 15 min. The samples are centrifuged at 10,000 x g for 20 min at 4°C. After centrifugation, RNA which is present in the aqueous phase is mixed with 10 ml of isoproponation and placed at 2-07°C for 1. The RNA precipitate is collected

by centrifugation, the pellet dissolved in 3 mt water and the RNA reprecipitated by addition of 1 volume of isocropnarol at 20°C. After centrifugation and washing the pellet in ethanol, the final pellet of RNA is dissolved in in water. The method yields approximately 300 µg of total cellular RNA. The final purified material is stored frozen at -20°C.

3.3 <u>lectation of poly(A) containing RNA:</u> Poly(A) containing RNA is selected from total RNA by chromatography on oligo(G17)-cellulose (Boehringer Mannheim) as described originally by Edmonds et al. (Proc. Natl. Acad. Sd. USA 68: 1335, 1971) and modified by Maniatis et al. (Medeular Coning: A Laboratory Manual, Cold Spring Harbor Laboratory, 1982, p. 197). The poly(A)-containing RNA is prepared as described in the published procedure with the exception that the RNA is eluted from the oligo(d17)-cellulose with water rather than SDS-containing buffer. The poly(A)-containing RNA is precipitated with ethanol and collected by centrifugation. The yield of poly(A)-containing RNA is approximately 30 μg from 300 μg of total cellular RNA. The final ourified material is stored frozen at 2-0°C.

Example 4. Cloning of functional heavy and light chain rearrangements from the FRP5 hybridoma cell line

Poly(A)-containing RNA isolated from FRP5 hybridoma cells as described in Example 3.3 provides the source for cDNA synthesis and subsequent amplification of V-region minigenes. Amplification products of the expected size are purified from agarose gels and cloned into appropriate vectors. Functional rearrangements are identified by sequencing.

4.1 Oligonucleotides:

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MCK2 is designed to be complementary to a region in the murine immunoglobulin κ (kappa) constant minigene.

5'- TCACTGGATGGTGGGAAGATGGA - 3'

MCHC2 is designed to be complementary to a region in the murine immunoglobulin γ1 constant minigene.

5'-AGATCCAGGGCCAGTGGATAGA-3'

The oligonucleotides VH1FOR, VH1BACK, VK1FOR, and VK1BACK are designed by Orlandi et al. (Proc. Natl. Acad. Sci. USA 86: 3833, 1989) to match consensus sequences.

VH1FOR: 5'-TGAGGAGACGGTGACCGTGGTGGTCCCTTGGCCCCAG-3'

VH1BACK: 5' - AGGT(C/G)(C/A)A(G/A)CTGCAG(G/C)AGTC(T/A)GG - 3'

VK1FOR: 5' - GTTAGATCTCCAGCTTGGT(c/G)C(C/G) - 3'

VK1BACK: 5' - GACATTCAGCTGACCCAGTCTCCA - 3'

4.2 <u>ODNA synthesis:</u> 55 ng of poly(A)-containing RNA is dissolved in a buffer containing 50 mM Tris-HCJ, HB 3.3 m Mm agnesium choirde, 10 mM DTT, 75 mM RCJ, 400 µM dNTPs (H= 6, A, T and C), 100 µg BSA (molecular biology grade, Boehringer Mannheim), 100 U RNAse inhibitor (Boehringer Mannheim), 25 pmol MCHC2. The RNA is denatured at 70° C for 5 min and then chilled on is 60 r 2 min. After addition of 200 U of MMLV reverse transcriptase (Gibco, BRL) cDNA synthesis is achieved by incubation for 1 h at 37°C.

4.3 <u>Polymerase chain reaction</u>: One tenth of the cDNA reaction is used for DNA amplification in buffer containing 10 mM Tris-HCl, pH 8.3, 1.5 mM MgCl₅, 50 mM KCl, 10 mM β-mercaptoethanol, 200 μM dNTPs (N= G, A, T and C), 0.05 % Tween-20[™] (Merck), 0.05 % NP-40[™] (Merck), 10 % DMSO (Merck), 25 pmol oligonuclectide 1 (see below), 25 pmol oligonuclectide 1 (see below), 25 pmol oligonuclectide 1 (see below), 25 pmol oligonuclectide 1 (see below) and 2.5 U Amplitaq[™] DNA polymerase (Perkin Elmer Cetus). Tan polymerase is added after intitle denaturation at 33 °C for 1 min and subsequent annealing at 37 °C. In the first 4 cycles primer extension is performed at 71 °C for 0.2 min, denaturation at 93 °C for 0.01 min and annealing at 37 °C for 0.2 min. For the last 25 cycles the annealing temperature is raised to 62 °C. Finally, amplification is completed by a 3 min primer extension step at 71 °C.

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	PCR Product	oligonucleotide 1	oligonucleotide
50	HC	MCHC2	VHIBACK
	Н	VH1FOR	VH1BACK
	LC .	MCK2	VK1BACK
55	L	VK1FOR	VK1BACK

4.4 <u>Modification and purification</u>: Amplified material is extracted with CHCl₃ and precipitated with ethanol in the presence of 200 mM LiCl. To facilitate cloning, blunt ends are created by a 3 min treatment with 1 U T4

DNA polymerase (Boehringer Mannheim) in 66 mM Tris-acetate, pH 7.9, 132 mM potassium acetate, 20 mM msgnesium acetate, 1 mM DTT, 200 µg/ml BSA (molecular biology grade, Boehringer Mannheim), and 400 µM dNTPs (H = G, A, T and C). The polymerase is inactivated by heatling for 15 min at 65°C before phosphory-lation of the DNA with 10 U T4 polymucleotide kinase (Pharmaccia) at 37°C for 1 h. For this purpose the buffer is adjusted to 50 mM EDTA and T MM ATP. The modified amplification products are separated on a 1.2% (w/w) agarose gel (ultra pure DNA grade agarose, Biorad) and DNA of the expected size is eluted by means of DEAE NA 45 membranes (Schleicher A Schuelf).

4.5 Ligation: Bluescript^{IM} KS+ (70 ng) linearized with Xbal, treated with Klenow DNA polymerase (Boshringer Mannheim) to give blunt ends and dephosphorylated with call finishing hlosphstase, and 30 ng of purified amplification product are ligated using 0.5 LI 74 DNA ligase (New England Biolabs) in 50 mM Tris-HCI, pH 7.8, 10 mM magnesium chindte, 10 mM DTT, and 0.8 mM ATP overnight at 19°C. One half of the ligation mixture is used to transform E. coll 1803 to obtain amplicilli resistant cidonies. These are screened for the desired ligation products using a NaOH based plasmid "miniprep" method (Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, 1982). The following plasmids are obtained:

	PCR product	Plasmid clones
	HC	pMZ15/1
•	Н	pMZ15/2 pMZ16/1
	L	pMZ16/2 pMZ17/1
	LC	pMZ17/2 pMZ18/I
5		pMZ18/2

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4.6 <u>Sequencing</u>: Sequencing is done using Sequenase™ kits (United States Biochemicals) with T3 and T7 oligonucleotide primers according to procedures provided by the manufacturer.

Plasmid pMZ17/1 contains a non-functional rearrangement. Plasmid pMZ 17/2 contains an Ig-unrelated sequence. Plasmids pMZ18/16/EG ID ND:2) and pMZ18/2 contain identical functional FRP5/appa light chain variable domain inserts. Plasmids pMZ16/1 contain pMZ16/2 contain identical functional FRP5 heavy chain variable domain inserts. Plasmids pMZ16/1 and pMZ16/2 contain FRP5 heavy chain variable domain inserts together with some constant region DNA. Plasmids pMZ16/1 and pMZ18/1 are used as a source for further subcloning steps.

Example 5. Construction of the MAb FRP5 single-chain Fv gene

For the construction of the cloning linker the 6 complementary oligonucleotides 1A, 1B, 2A, 2B, 3A, 3B are used.

- 1A: 5'-CAAGCTTCTCAGGTACAACTGCAGGAGGTCACCGTTTCCTCTGGGG-3'
- 1B: 5'-GAAACGGTGACCTCCTGCAGTTGTACCTGAGAAGTCTTGCATG-3'
 - 2A: 5'-TGGCGGTTCTGGTGGCGGTGGCTCCGGCGGTGGCGGTTCTGAC-3'
 - 2B: 5'-GCCACCGCCGGAGCCACCGCCACCAGAACCGCCACCGCCAGAG-3'
 - 3A: 5'-ATCCAGCTGGAGATCTAGCTGATCAAAGCT-3'
 - 3B: 5'-CTAGAGCTTTGATCAGCTAGATCTCCAGCTGGATGGATGTCAGAACC-3'
- 40 pM of oligonucleotides 1B, 2A, 2B, 3A are phosphorylated at the 5' end using T4 polynucleotide kinase (Boehinger Mannheim) in four separate reactions in a total volume of 20 µ following the method described by Maniatis et al. (Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, 1982). Oligonucleotides 1A and 3B are not phosphorylated in order to avoid self-lication of the linker in the final lication reaction.

After the kinase reaction, the enzyme is inactivated by incubation at 70°C for 30 min. In three separate reactions, each containing 40 pM of two oligonucleotides in a total volume of 40 µl, non-phosphorylated 1A and phosphorylated 1B, phosphorylated 2A and phosphorylated 2B, and phosphorylated 3A and non-phosphorylated 3B are mixed. Hybridization of the oligonucleotides in the three reactions is carried out by heating to 95°C for 5 min, incubation at 65°C for 5 min and slowly cooling to room temperature. 10 µl from each of the three reactions are mixed, 4 µl of 10 x ligation buffer (Boehringer) and 4 units of T4 DNA ligase (Boehringer) are added and the total volume is adjusted to 40 µl with sterile water. The annealed pairs of oligonucleotides are ligated into one linker sequence for 16 h at 14°C. The reaction mixture is extracted with an equal volume of phenol/chloroform (1:1) followed by re-extraction of the aqueous phase with an equal volume of chloroform/isoamylalcohol (24:1). The aqueous phase is collected, 0.1 volumes of 3 M sodium acetate pH 4.8 and 2 volumes of ethanol are added, and the DNA is precipitated at -70°C for 4 h and collected by centrifugation. The resulting linker sequence has a SphI and a XbaI adaptor end. It is ligated to SphI and XbaI digested pUC19 in a reaction containing 100 ng of ligated linker and 200 ng of Sphl/Xbal digested pUC19. After transformation into E. coli XL1 Blue™ (Stratagene), plasmid DNA from 4 independent colonies is isolated by the alkaline lysis mini-preparations method (Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, 1982). The DNA sequence of the linker cloned in pUC19 is determined by sequencing double stranded DNA in both directions with Sequenase II (United States Biochemicals) and pUC universal and reverse primers (Boehringer) following the manufacturer's protocol. Three out of the four recombinant pUC 19 isolates sequenced contain the correct linker sequence. One of them is designated pWW 19 and used in the further experiments. The sequence is shown in SEQ ID NO:3.

5.2 Preparation of a plasmid for the subcloning of variable domains: The Fv cloning linker sequence is derived as a 144 bp HindIII/SacI fragment from pWW19 and inserted into HindIII/SacI digested Bluescript™ KS+ (ex Pvull) (Stratagene) which contains no Pvull restriction sites. The resulting plasmid, pWW15, allows cloning of heavy and light chain variable domains as Pstl/BstEII and Pyull/BstIII fragments, respectively.

5.2.1 Subcloning of the FRP5 heavy chain variable domain: Plasmid pMZ16/1 is digested with Psti and BstEll and the 338 bp heavy chain variable domain fragment of FRP5 is isolated. It is cloned into PstI/BstEll digested pWW19 yielding the plasmid pWW31.

5.2.2 Mutation of the FRP5 light chain variable domain and assembly of the Fv fusion gene: To facilitate subcloning of the FRP5 light chain variable domain into the Fv cloning linker, a Pyuli restriction site and a Bglll restriction site are introduced at the 5' and 3' ends, respectively, of the coding region. The FRP5 light chain variable domain coding region is isolated as a Sacl/BamHI fragment from pMZ18/1. Sacl and BamHI are restriction sites of the Bluescript™ polylinker present in pMZ18/1. The fragment contains the complete light chain variable domain fragment of 392 bp amplified by PCR using the oligonucleotide MCK2 (see above). This fragment is mutated and amplified by PCR using the oligonucleotides

V.5':5'-GACATTCAGCTGACCAG-3' and

V.3':5'-GCCCGTTAGATCTCCAATTTTGTCCCCGAG-3'

for the introduction of a Pvull restriction site at the 5' end (VL5') and a Bolll restriction site at the 3' end (V,3') of the kappa light chain variable domain DNA, 20 ng of the FRP5 variable light chain Saci/BamHI fragment are used as a template in a 100 µl reaction following the PCR conditions described in Example 4.3. The amplified and mutated fragment is isolated after Pvull/Bglll digestion as a 309 bp fragment from a 1.5 % agarose gel and cloned into Pyull/BgIII digested pWW15 generating plasmid pWW41. The FRP5 kappa light chain variable domain is isolated as a BstEll/Xbal fragment from pWW41 and inserted into BstEll/Xbal digested pWW31. Thus the FRP5 heavy chain variable domain in pWW31 and the FRP5 kappa light chain variable domain are fused to one open reading frame. Double stranded DNA of three independent clones is sequenced with Sequenase 45 II™ kit (United Biochemicals) in both orientations using pUC universal and reverse primers (Boehringer) following the manufacturer's protocol. One of the plasmids carrying the FRP5 heavy chain variable domain fused to the mutated FRP5 light chain variable domain is selected and designated pWW52. The sequence of the HindIII/Xbal insert in plasmid pWW52 is shown in SEQ ID NO:4.

Example 6. Construction of a single-chain Fv-phosphatase fusion gene expression plasmid

The MAb FRP5 single-chain Fy gene is fused to the bacterial alkaline phosphatase. This chimeric gene encodes a bifunctional molecule which retains binding activity to the c-erbB-2 protein and has enzymatic activity.

6.1 Mutation of the single-chain Fv(FRP5) gene: To allow gene fusion between the single-chain Fv(FRP5) encoding gene from pWW52 and the alkaline phosphatase gene phoA the stop codon at sequence position 729 to 731 in pWW52 (see Example 5.2.3) is deleted as follows: Plasmid DNA of pWW52 is digested with BstEll and BgIII and the linker sequence and FRP5 light chain variable domain encoding fragment is isolated. In

another digestion, pWW52 is cleaved with BstEII and BcII. Thus, the large fragment containing vector sequences and the FRP5 heavy chain variable domain encoding sequence is isolated. The BstEII/BgIII V, fragment is now inserted into BstEII/BcII cleaved pWW52 containing V_{Ir}. In the resulting plasmid, pWW53, the BgIII/BcII junction is determined by sequencing double stranded DNA as described above.

Sequence of the BgllI/Bcll junction in pWW53 (position numbers correspond to position numbers of the HindllI/Xbal insert in plasmid pWW52, SEQ ID NO:4):

BelII/BelI

ACA AAA TTG GAG ATC AAA GCT CTA GA 714-728 | 738 - 748

6.2 Mutation of the E.coli alikaline phosphatase gene phoA: For the construction of the FV(FRP5-)-phoA fusion gene the E.coli alikaline phosphatase gene phoA is mutated to generate a Xhat cleavage site in the coding region of phoA near the N terminus of the mature protein and a Sacl cleavage site in the 3' untranslated region of phoA. This step facilitates the cloning of the mutated fragment A pBR322 derivative carrying the recombinant transposon TnPhoA (Manol & Beckewith, Proc. Natl. Acad. Sci. USA 82 8129, 1985) is linearized by Bgill cleavage. 20 ng of the linearized template DNA is used for a 100 µ PCR reaction carried out as described previously using oligonucleotides PhoA5' and PhoA5' as primers 1 and 2.

PhoA5':5'-CCCTCTAGAGCCTGTTCTGGAAAAC-3'
PhoA3':5'-CCCGAGCTCTGCCATTAAG-3'

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Following Xbal/Sacl digestion of the PCR products, a 1419 bp fragment is isolated from a 1.5 % agarose gel and inserted into Xbal/Sacl digested plasmid pUC19. Ligation is carried out as described above. Ligated DNA is transformed into £_coil X.1 Blue*" (Stratagene). Thus, the open reading frame of the ruitated phoA gene is fused in frame to the leaC open reading frame of pUC19. To show that the mutated phoA gene expresses incitional atlaitine phosphatases, recombinant clones are plated onto LB ager plates containing 100 µg/ml ampicitin, 0.5 mM IPTG (Sigma), and 40 µg/ml XP (Boehringer). Following induction of the lac promoter of pUC 19, a lacZ-phoA fusion protein is expressed. The phosphatase activity of this fusion protein converts the indicator XP to a blue dye. One of the blue colonies is soliated and the presence of the introduced restriction sizes is confirmed by digestion of rimitiprep DNA with Xbal and Sacl. Partial 5' and 5' DNA sequences of the mutated phoA gene are obtained by sequencing double stranded DNA as described above. The DNA sequences are included in the assembly of the final FV(FRP5)-phoA fusion gene sequence shown in SEQ ID NO:5. The isolated plasmid is designated pWW45 and used for further subcloning steps.

6.3 Construction of a FRP5 Fv-phoA expression plasmid: From plasmid pWW19 (see Example 5.1.2) the cloning linker sequence is isolated as a Hindill/EcoRl fragment and inserted into Hindill/EcoRl fragment plasmid plNIII-ompA-Hind (Rentier-Delrue et al., Nucl. Acids Res. 16: 8726, 1998) leading to plasmid pWW16.

From pWW61 (see Example 6.2) the mutated phoA gene is isolated as a XballSad fragment and Inserted into Xball/Sad digested pWW53. The resulting plasmid, pWW615, carries the Fv(FRP5) gene fused in frame to the mutated alkaline phosphatase gene. The Fv(FRP5)-phoA gene is lociated as a Hindill/Sad fragment from pWW615 and inserted into Hindill/Sad digested plasmid pWW16. This leads to the production of the Fv(FRP5)-phoA expression plasmid pWW616 (see below). All ligations are carried out as described above. Recombinant plasmids are transformed into E. coll XL1 Blue™ (Stratagene). The constructs are confirmed by restriction enzyme analysis of plasmid DNA isolated by an alkaline mid proparation method (Maniatis et al., Molecular Coning: A Laboratory Amunul, Cold Spring Harbor Laboratory, 1992).

In this construct the Fv single-chain antibody of FRP5, genetically fused to the alkaline phosphatase phoA, can be expressed in E. coli following induction with IPTG. The recombinant protein carries the E. coli outer membrane protein A (ompA) signal sequence at the N terminus (encoded by the pINIII-ompA-Hind vector) to facilitate secretion of the protein into the periplasmic space of E. coli expressor cells.

The sequence of the Fv(FRP5)-phoA fusion gene in expression plasmid pWW616 is shown in SEQ ID NO:5. Part of the phoA sequence is assembled from Chang et al., Gene 44: 121, 1986.

Example 7. Expression of Fv(FRP5)-phoA in E. coli

Plasmid pWW616 is transformed into the phoA negative <u>E. coli</u> strain CC118 (Manoil & Beckwith, Proc. Natl. Acad. Sci. USA 82. 8129, 1985). A recombinant single colony is grown overnight in 50 m LB medium containing 70 μg/ml ampicillin. The overnight culture is diluted 1:10 in 500 ml fresh LB medium containing 70 μg/ml ampicillin and grown at 37°C to an OD₂₀ of 0.1. IPTG is added to a final concentration of 2 mM and exp-

ression is induced for 1.5 h at 37°C. The cells are harvested at 4°C by centrifugation at 4000 rpm for 25 min in a Beckman GPKR centrifuge. The supermantant of CC118/pWW616 is set aside on ice for preparation of FV(FRP5)-phoA, see Example 7.2.

- 7.1 isolation of Fy(FRPS)-phoA from the periplasmic proteins of CC118pWW616: The bacterial pellet is suspended in 10 mTES buffer (Q.2 M Tris+HC1, Ph.8.0, 0.5 mM BDT7, 0.5 M surces) and kept no lee for 10 min. After centrifugation at 4°C for 10 min at 5000 rpm in a Heraeus minifuge, the supernatant is discarded and the washed pellet is suspended in 15 ml ice-cold TES, dituted (1.4) with water. The cells are kept on loe for 30 min and recentrifuged as above. The supernatant containing periplasmic proteins is recentrifuged at 45,000 xg for 15 min in a Beckman TL100 ultracentrifuge. The periplasmic extract is concentrated in an American ultraffictation until through a YM10 membrane five times, the 1.4 dituted TES buffer of the periplasmic extract is exchanged with PBS. NaN, and proteinse inhibitors are added to the periplasmic contains (2 ml in PBS) to the final concentration of 0.02 % NaN, o. 1 mM PMSF, 2 µg/ml aprotinin, 1 µg/ml leupeptin, and 1 µg/ml pepsitain. The periplasmic contact is stored at 4°C1.
- 7.2 [solation of Fw(FRP5)-phoA from the concentrated supernatant of E_coil CC118/pWW816 outbres: The supernatant (500m) of the induced E_coil culture CC118/pWW816 is filtered through a 0.45 µm membrane. The filtrate is concentrated in an Amicon ultrafiltration until through a YM10 membrane to a final volume of 10 ml in PBS as described above. NaN₂ and protease inhibitors are added to the concentrated supernatant to the final concentrations indicated above. The concentration of Fv(FRP5)-phoA in the extracts is determined by denstrometry in comparison to BSA standards of coomassie stained 9 % SDS-PAGE gels.

Example 8. Activity of Fv(FRP5)-phoA

- 8.1 <u>Detection of c-erb8-2 in SKBR3 breast tumor cells by immunostaining using Fv(FRP5)-phoA:</u> The Fv domain of Fv(FRP5)-phoA enables the molecule to bind to the extracellular domain of the c-erb8-2 protein. Bound Fv(FRP5)-phoA can be visualized by staining procedures using color substrates for the detection of alkaline phosphatase activity.
 - 8.1.1 Fixation of cells: SKBR3 human breast tumor cells carrying about 1 x 10° c-erb3-2 meoptors per cell are grown on fibronectin coated glass cover slips. The cells are washed twice with PBS and then fixed with PBS 13.7 % formaldehyde at room temperature for 30 min. The fixed cells are washed three times with PBS at room temperature. Unspecific binding sites are blocked by incubating the cells for 1 h with PBS / 3 % BSA at 37°C in a humid incubator. The cells are then washed whice with PBS.
- 8.1.2 Pretreatment of FV(FRPS)-phoA: Alkaline phosphatase phoA from E. coll must be dimerized to be enzymatically active. In the periplasm of E. coll natural phoA is dimerized, i.e. two molecules of phoA are held together by two Zr?* fors. The FV(FRPS)-phoA is also produced as a dimer in E. coll. To increase binding of FV(FRPS)-phoA to the antigen, the dimers are monomerized by adding EGTA to the solution. This step removes Zr?* from the solution. Monomerized phosphatase can be re-dimerized by the addition of Zr?* EGTA is added to a final concentration of 5 mM to 200 µl of 40 x concentrated supermatant or periplasmic proteins from CT18/pWWRST6 (see above). The solution is inclusted at 3T° Cor 1 h is better cue sein the immunosasary.
- 8.1.3 Staining of cells: After blocking with PBS / 3 % BBA (see above) fixed cells are incubated for 1 h with prefreated FV(FRP5)-pibo At a concentration of 1 µgml at 37°C in a hundified incubator. The cells are washed three times with PBS at room temperature. The staining solution consists of 300 µl naphtol AS-MX** phosphate (Sigma, 13 mg/ml in dimethyl formamide), 8 mg of levamisole (Sigma), and 10 mg of Fast Red TR** satt (Sigma) added to 9.7 ml of 100 mM Tris-HCl, PH 8.2, 1 mM ZnCl₂. This mixture is prepared and filtered through a 0.45 µm filter immediately before use. ZnCl₂ is added to the staining solution to allow re-dimetration of bound FV(FRP5)-phoA and thereby activating the alkaline phosphatese. Cells are incubated in the Fast Red **Staining solution for 15 min at room temperature. The phosphatese activity is blocked after staining by washing the cells wise with PBS and once with 1 M5/FpC, (Bass cover sitips are mounted with get mount (Simeda). The cells are examined under a fluorescence microscope using green light for excitation. Stained SKBR3 cells show intense red cell surface fluorescence.
- 8.2 Detection of c-erb8-2 protein over-expression in immunoblots using Fv(FRP5)-phot. Proteins from total cell systes of SKBR3 cells over-expressing c-erb8-2 protein are separated by SDS-PAGE and blotted onto PVDF membrane (Milliproe). For preparation of extracts and immunoblotting technique see Example 1.3.2. Free binding sites of the membrane are blocked by incubation for 1 h at room temperature in a solution containing 10 mM Tris-HCl, PH.7.5, 0.9 % NaCl, 0.0.5 % Tween 20° (BloRad), and 3 % BSA. Pretreated Fv(FRP5)-phoA (see Example 7.2.) is diluted in blocking solution to a final concentration of 0.1 µg/ml. The membrane is incubated in the Fv(FRP5)-phoA solution for 1 h at room temperature and then washed three times for 5 min at room temperature in 10 mM Tris-HCl. Ph.7.5, 0.9 % NaCl, 0.05 % Tween 20° M; Tween 20° min donce in 10 mM Tris-HCl.

pH 7.5, 0.9 % NaCl. For detection of bound Fv(FRP5)-phoA the membrane is incubated for 20 min at 37°C in the Fast Red™ substrate solution described in Example 7.3 without levamisole. The reaction is stopped by washing the membrane twice in water. Fv(FRP5)-phoA specifically detects the 185 kD c+afbB-2 protein.

Example 9. Expression and isolation of Fv(FRP5)-phoA from E. coli

- 9.1 <u>Preparation of periplasmic extract</u>: Plasmid pWW616 is transformed into the phoA negative <u>E. coli</u> strain CC118 according to standard procedures (Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, 1982). A single colony is picked and grown overnight in LB medium containing 70 µg/ml ampicillin. The overnight culture is diluted 1:10 in fresh LB medium containing ampicillin and grown at 37°C to an Ob₂₀₀ of 1.4 this point expression of the FV(FRP5)-phoA gene is induced by the addition of IPTG to a final concentration of 2 mM, and the cells are grown for an additional 1.5 to 2 h. The cells are harvested by centrifugation and treated with a mild osmotic shock which releases the periplasmatic proteins into the supernatant. The proteins are concentrated in an American ultrafiliation until through a YM10 membrane and the supernatant. The proteins are concentrated in an American ultrafiliation until through a YM10 membrane.
- 9.2 Preparation of an antigen affinity coturn. The c-erbB-2 protein is lecitated from insect cells infected with a baculovirus vector expressing the c-erbB-2 extracellular domain by standard methods (V.A. Luckow & M.D. Summers, Biotechnology 6: 47-55, 1986), MAb FSP77 is coupled to CNBR-activated Sepharose 48° (*Pharmacia) following the instructions of the manufacturer. The insect cell lysates are incubated with the coupled MAb FSP77 in a buffer containing 50 mM Tin-ERC, pt 7.5, 5 mM BCGT0, 0.5 % TINOT X-100° 1,50 mM NaCl for 2 h at 4°C on a shaking platform. The beads are packed into a column and washed with pre-elution buffer consisting of 10 mM plnopshape, pt 8.3, and 100 mM NaCl to remove non-specifically bound proteins. The c-erbB-2 protein is recovered from the column are officially bound proteins. The c-erbB-2 protein is recovered from the column are officially bound proteins. The c-erbB-2 protein is recovered from the column are officially bound proteins. The c-erbB-2 protein is recovered from the column are officially protein proteins of the column are officially part of each fraction on 8 % SDS-PAGE gel, blotting onto PVDF membrane (Millipore) and treating the filter with MAb FSP77 followed by sheep anti-mouse IgG. Bound IgG is detected by "IsP-Protein's fractions containing the extracellular domain are pooled and the protein is coupled to CNBR-activated Sepharose 48TM (Pharmacia) following the Instructions of the manufacturer.
- 9.3 <u>Isolation of Fv(FRP5)-phoA by affinity chromatography</u>: The sepharose coupled to c-erbB-2 protein (Examle 9.2) is incubated for 2-4 h at 4°C on a rocking platform with the periplasmic extract isolated as described in Example 9.1. The beads are packed into a column and washed with pre-elution buffer as in Example 9.2. The Fv(FRP5)-phoA protein is recovered by elution with the low pH elution buffer of Example 9.2. The fractions are monitored for the presence of the Fv(FRP5)-phoA by testing for phoA enzymatic activity using a standard protocol.

Example 10. Immunoassay for c-erbB-2 protein in tumors

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- 10.1 Preparation of tumor sections: To determine the level of o-erb8-2 protein in tumors, tumor tissue is pretreated to give either frozen tumor sections or paraffin-embedded tumor sections. Tumor pieces are quick frozen, then cut with a cryostat, collected onto 1% gelatin-coated glass sides, and fixed with 4% paraformal-dehyds. Following several washes with PBS, the tumor tissue sections are ready for staining. Alternatively, tumor pieces are pleaded in 4% paraformaled/yels for fixation, embedded in parafin, then sections out and collected onto polytysine-coated glass cover slips. To prepare the sections for staining, they are heated overnight at 56°C, dewaxed in xylene, stepwise rehydrated by washing in 95 %, 70 % and 35 % ethanol and water, and washed in PBS.
- 10.2 Pretreatment of Fv(FRP5)-phoA. Since the dimer of the Fv(FRP5)-phoA as obtained from the E. coil periplasm does not bind optimally to the c-erb8-2 radigen, it is first monomerized. This is accomplished by treating the solution of Fv(FRP5)-phoA for 1 hat 37°C with EGTA at a final concentration of 5 mM. This treatment chelates the Zn** from switch are important for maintaining the dimeri structure of VF(FRP5)-phoA.
- 10.3 Staning of the tumor sections: Non-specific staining of the tumor sections prepared according to Example 10.1 is blocked by inclusibing the sections in PBS containing 3 % BBA. The blocked sections are incubated for 1 - 2 h with pretreated FwFRP5-phoA. (Example 10.2) at a concentration of 1 upin In a humidified chamber at room temperature. The sections are washed three times with PBS at room temperature. The bound Fv(FRP5-phoA protein is detected using Fast Red¹⁴⁴ as a substrate for the alkaline phosphatase. The staining solution consists of 300 µl naphthol AS-MX phosphate (Sigma, 13 mg/ml in dimethylformamide), 8 mg of levanisicle (an inhibitor of endogenous alkaline phosphatase, Sigma), and 10 mg of Fast Pated TR* salt (Sigma) added to 9.7 ml of 100 mM Tris-HCl, pH 8.2, and 1 mM ZnCl₂. This mixture is prepared and filtered through a 0.45 um filter immediately before use 2.70L; is added to the staining solution to allow re-dimetrization of the bound

Fv(FRPS)-phoA protein and activation of the alkaline phosphatase. The lumor sections treated with Fv(FRPS)phoA are incubated in the Fast Red[™] staining solution for 15 min at room temperature. After staining the phosphatase activity is blocked by washing the cells twice with PBS and once with 1 M KH₂PO₄. The glass cover slips are mounted with gel mount. The cells are examined under a fluorescence microscope using green light for exclation, Positivel visatine doel show an intense red cell surface fluorescence.

Alternatively, the turnor sections treated with the FVFRP5-phoA protein may be stained with naphthol AS-Bl phosphate S(Sigma) and Niev Fuchsin** (Sigma), or with 5-bromo4-chloro-2-indoyl phosphate (BCIP, Sigma) and Nitro Blue Tetrazolium** (Sigma). The stained sections can then be viewd with a regular light microsonce.

Example 11. Cloning of functional heavy and light chain rearrangements from the FWP51 hybridoma cell line

Poly(A)-containing RNA isolated from FWP51 hybridoma cells as described in Example 3.3 provides the source for cDNA synthesis and subsequent amplification of V-region minigenes. cDNA synthesis and amplification of FWP51 heavy and light chain variable domain cDNA by oplymerase chain reaction is carried out as described in Example 4. Amplification products of the expected size are purified from agarose gels and cloned into appropriate vectors. Functional rearrangements are identified by sequencine.

11.1 Subdoning of FWP51 heavy and light chain variable domain cDNA, Material amplified according to Example 4.3 is extracted with CHCl₃ and precipitated in the presence of 200 mM LiCl. To facilitate cloning, the FWP51 heavy chain variable domain cDNA is cleaved with restriction enzymes Petl and BstEll, the fragment purified by agarose gel electrophorosis, and ligated to PstI and BstEll digested pWW15 DNA. The FWP51 light chain variable domain cDNA is cleaved with restriction enzymes Pvull and BglII, the fragment is purified by agarose gel electrophoresis, and ligated to Pvull and BglII digested pWW15 DNA (cf. Example 5). Ligation, transformation, and screening for the desired ligation products are carried out as described in Example 4.5. The following plasmids are obtained:

	PCR product	Plasmid clones
,	H	pWW15-VH51-1
		pWW15-VH51-2
		pWW15-VH51-3
5		
	L	pWW15-VL51-1
		pWW15-VL51-2
		nWW15_VI 51_3

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11.2 Sequencing: Sequencing is done as described in Example 4.6.

Plasmids pWW15-VH51-1 (SEQ ID NO:6), pWW15-VH51-2, pWW15-VH51-3 contain identical functional FWP51 heavy chain variable domain inserts. Plasmids pWW15-VL51-1 (SEQ ID NO:7), pWW15-VL51-2, pWW15-VL51-3 contain identical functional FWP51 kappa light chain variable domain inserts. Plasmids pWW15-VH51-1 and pWW15-VL51-1 are used as a source for further subcloning steps.

Example 12. Construction of the MAb FWP51 single chain gene

- 12.1 <u>Assembly of the Fv fusion gene</u>: Plasmid pWW15-VH51-1 is digested with Pstl and BstEil and the 35 by heavy chair variable domain fragment of FWP51 is isolated. It is cloned into Pstl/BstEil digested pWW15-V-51-1 yielding the plasmid pWW15-V-51-5 (SEQ ID NO: 8).
- 12.2 <u>Mulation of the single-chain FvfFWP51) gene</u>: To allow gene fusion between the single-chain FvfFWP51 and effector genes the stop codon at sequence position 729 to 731 in pWWFvf5-51 (SECII DNO:8) is deleted as follows (see also Example 6.1): plasmid DNA of pWWf5-Fv51 is digested with BatEII and BBII and the linker sequence and FVPF1 light chain variable domain encoding fragment is isolated. In another digestion, pWWf5-Fv51 is cleaved with BatEII and BBII. Thus, the large fragment containing vector sequences and FVPF5 is the development of the Section of the Section 1.

BstEll/Bglll VL fragment is now inserted into BstEll/Bdl cleaved pWW15-Fv51 containing V_H. The resulting plasmid pWW15-Fv51-ORF is used as a source for the construction of Fv(FWP51)-effector fusion genes.

Example 13. Construction of single-chain Fv-exotoxin A fusion gene expression plasmids

The MAb FRP5 and MAb FWP51 single-chain Fv genes are fused to a truncated bacterial toxin, exotoxin A (ETA) from Pseudomonas aeruginosa. These chimeric genes encode recombinant immunotoxins which selectively inhibit protein synthesis in c-er0F2-expressing cells.

13.1 Mutation of the Exotoxin A gene of Pseudomonas aeruginosa PAK: For the construction of Fv-exotoxin A (Fv-ETA) fusion genes the ETA gene from Pseudomonas aeruginosa PAK is mutated to delete the original cell binding domain I at the N-terminus of the toxin and to generate a Xbal cleavage site at the former domain I/domain II boundary of the ETA coding region. Plasmid pMS150A (Lory et al., J. Bacteriol. 170: 714, 1988) is linearized by EcoRI cleavage. 20 ng of the linearized template DNA is used for a 100 µl PCR reaction carried out as described previously using the following oligonucleotides as primers 1 and 2.

1: 5'-CACGGAAGCTTAAGGAGATCTGCATGCTTCTAGAGGGCGGCA-

GCCTGGCCGCGCTG-3'

2: 5'-GCGGATCGCTTCGCCCAGGT-3'

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Following HindIII/Sall digestion of the PCR products, a 201 bp fragment is isolated from a 1.5% agarose gland inserted into HindIII/Sall digested plasmid pUC16. Ligation is carried out as described above. Ligated DNA is transformed into E.coll XL1 Blue TM (Stratagene). Two recombinant plasmids are isolated and the insert DNA is sequenced as described above using pUC universal and reverse primers (Boehiniger). One plasmid containing the expected product is designated pWW22 (SEQ ID NC.9) and used as a source for further sub-cloning steps. Plasmid pWW22 is cleaved with HindIII and Sall, the mutated ETA gene fragment is isolated, and inserted into the larger fragment of HindIIIISall digested plasmid pMS150A containing pUC9 vector sequences and part of the ETA gene coding for the C-terminal half of the toxin. Thereby in the resulting plasmid pWW20 at functed ETA gene coding for dwarfs. Il and III of the toxin is created.

13.2 Assembly of single-chain Fv-ETA fusion genes: HindIII/Xbal single-chain Fv gene fragments suitable for the construction of Fv-ETA fusion genes are located from plasmid pWW35 (single-chain Fv FRPS), and plasmid pWW15-Fv51-ORF (single-chain Fv FWPS1) and inserted into HindIII/Xbal digested pWW20. Ligation and transformation into Ecol IXI. Blue "(Strategane) are carried out as described above. The resulting plasmids pWW20-Fv5 (Fv(FRP5)-ETA) and pWW20-Fv51 (Fv(FWP51)-ETA) are used as a source for further subcloning steps.

13.3 Construction of single-chain Fv-exotoxin A fusion gene expression plasmids: For the expression of single-chain Fv-exotoxix A fusion genes in Ecoli the expression plasmid pFLAG-f (IBI Biochemicals) is used. The fusion-genes are fused in frame to the outer membrane protein A (cmpA) signal sequence encoded by pFLAG-f. Plasmid DNA from pWW2D-Fv5 and pWW2D-Fv6 if digested with Hindfill and blunt endar ser created as by Vienorw fill-in as described above, the surgical 4.5 limits endar protein FV-ETA gene fragments are isolated (FV(FXPS)-ETA: 1916 bp., FVFWPS1) ETA: 1916 bp), pFLAG-i plasmid DNA is digested with EcoRI. Blunt-end/EcoRI Fv-ETA fusion gene fragments are inserted into the modified pFLAG-i plasmid DNA is digested with EcoRI. Blunt-end/EcoRI Fv-ETA fusion gene fragments are inserted into the modified pFLAG-i plasmid DNA. Thereby Fv-ETA fragments are issend in frame to the ompA signal sequence of pFLAG-1 creating plasmids pWW215-5 for the expression of FV(FWPS)-ETA (SEQ ID NO: 11).

Example 14. Expression and isolation of Fv(FRP5)-ETA and Fv(FWP51)-ETA from E. coli

14.1 Preparation of total lysates; Plasmids pWW2155 and pWW21551 are transformed into the E.coil strain CC118 according to standard procedures (see Example 9.1). Single colonies are picked and grown overnight in LB medium containing 100 µg/ml ampicillin and 0.4% glucose. The overnight cultures are dituted 1:30 in fresh LB medium containing ampicillin and glucose and grown at 37°C to an OD₂₅₀ of 0.5. At this point expression of the FVFRP5)=Tta Am FVFRY951-Tta Genes is induced by the addition of IPTG to a final concentration of 0.5 mM, and the cells are grown for an additional 30 min. The cells are harvested by centrifugation and lysed by sonication in PBS/1 mM CaCl₂. The lysates are cleared by ultracentrifugation at 25 000 g for 45 min at 4°C. The supermatants are collected.

14.2 Isolation of Fv(FRP5)-ETA and Fv(FWP51)-ETA by affinity chromatography. Cleared E.coli lysates containing the 66.4 MoB Fv(FRP5)-ETA or the 66.3 kDa Fv(FWP51)-ETA protein are passed through a l/1 monocdonal antibody affinity column (Bi Biochemicals). The column is washed three times with PBS/1 mM CaCl₂. Bound Fv(FRP5)-ETA or Fv(FWP51)-ETA proteins are eluted with PBS/2 mM EDTA. The fractions are monitored for the presence of Fv-ETA proteins by SDS-PAGE and immunoblotting (see Example 1.3.2) using an anti-exploxin A antiserum developed in rabity.

Example 15. Selective inhibition of protein synthesis in c-erbB-2 expressing cells with Fv(FRP5)-ETA and Fv(FWP51)-ETA

In vitro the recombinant immunotoxins Fv(FRP5)-ETA and Fv(FvVP51)-ETA selectively inhibit protein synthesis and growth of cells expressing high levels of the human c-erbB-2 protein. The immunotoxins do not affect cells expressing no, or low levels of human c-erbB-2 protein.

15.1 Immunotoxin treatment of cell lines: Human breast and ovarian tumor cell lines SK-BR3, MDAMB-231, MDA-MB-431, HTB77, the mouse marmary epithesial cell line HC11, and HC11 cells transfected with the human c-erb8-2 cDNA are plated on 48 well tissue culture plates (Costar) at a density of 105° cells/well. After 4 hthe medium is removed and replaced by normal growth medium containing PK/FRP9-ST-LA or FK/FWP51-ST-A or FK/FWF51-

15.2 <u>11-leucine labeling of cells</u>: The immunotoxin-treated cells are washed twice and incubated in normal growth medium containing 4 pcll*-ll-eucin/ mil or 4. The labeled cells are washed twice and 11-leucine labeled total proteins are harvested by TCA precipitation onto Whatman GFC filters. The rate of protein synthesis in immunotoxin-treated cells is determined in comparison to untraeded control cells.

Example 16: Fv(FRP5)-ETA and MAbs FWP51 and FSP77 inhibit the growth of c-erbB-2 expressing cells in nude mice.

The administration of Fv(FRP5)-ETA and the MAbs FWP51 and FSP77 to animals injected with c-erbB-2 expressing cells inhibits the tumor growth of these cells.

16.1 Nude mouse lumor model.: The NIH/3T3 mouse fibroblast cell line is transfected according to conventional, previously described methods (Graham & van der Et, Virology 52.4 Si, 913) with a plasmid expressing the point mutated, activated human c-erbB-2 protein (Masuko et al., Jon. Cancer Res. 80. 10, 1989) and with the plasmid pSV2neo (Southem & Berg, J. Mol. Appl. Genet. 1:327, 1982) which encodes the gene for resistance to the drug G418. Transfected cells are selected 2 weeks in medium containing 500 ug/ml G418 (Geneticin, Gibco-BRL), Individual clones are selected and analyzed for the expression of the human c-erbB-2 protein using conventional protein bioding schoriques (Towlin et al., Proc. Natl. Acad. Sci. USA 76: 4350, 1979). A done expressing moderate levels of the point mutated, activated human c-erbB-2 protein (clone 3.7) is selected, and tested for growth in unde mice. 2-5x 106 clone 3.7, cells (per animal) suspended in C2 ml PBS are subcutaneously injected into the flank of female Balb/c nude mice. The 3.7 cells injected at a dose of 2 x 106 cells replied from tumors in under mice control animals, cf. Example 16.2)

16.2 Immunotoxin treatment of animats; 2x 106 done 3,7 cells are injected subcutaneously into nude mice. The animals are treated continuously for a total of 7 days with the Fv(FRP5)-ETA, 200 µl of Fv(FRP6)-ETA (concentration 35 µg/ml in PBS) is placed in an osmotic pump (Alzet mind osmotic pump, Model 2001, Alza, Palo Alto, CA, #94303-0902) which is implanted subcutaneously into the animals at the same time as the done 3.7 cells are injected. The pump continuously releases Fv(FRP5)-ETA and delivers 1 µg/day for 7 days to each animal. In comparison with the control animals (cf. Example 16.1), the administration of Fv(FRP5)-ETA delays the onset of tumor formation.

16.3 MAb treatment of animals: 5 x 106 done 3.7 cells are injected subcultaneously into nude mice. Starting on the same day as injection of done 3.7 cells, he animals are treated daily, for a total of 10 days, with either MAb FWP51 or MAb FSP77 (MAb dose is 50 ug/200 ul BSS/day). The MAb is injected intraveneously in the tal vieri of the mouse. Both antiblodies delay the conset of tumor growth. Compared therewith, a synergistic effect in inibibiliting tumor growth is observed on simultaneous administration of both antibodies MAb FWP51 and MAb FSP77.

30

Sequence listing

5 SEO ID NO:1

35

50

55

SEQUENCE TYPE: nucleotide
SEQUENCE LENGTH: 361 bp
MOLECULE TYPE: plasmid DNA
ORIGINAL SOURCE ORGANISM: mouse
IMMEDIATE EXPERIMENTAL SOURCE: E. coli
NAME OF CELL CLONE: pMZ16/1

 75
 FEATURES: from 6 to 27 bp from 95 to 109 bp from 95 to 109 bp from 152 to 202 bp from 299 to 328 bp from 299 to 338 bp from 299 to 361 bp
 VH1BACK primer region CDR_{1H} CDR_{2H} CDR_{2H}

- PROPERTIES: encodes the heavy chain variable domain of monoclonal antibody FRP5
- TCTAGAGGTG AAACTGCAGC AGTCTGGAGC TGAACTGAAG AAGCCTGGAG 50

 AGACAGTCAA GATCTCCTGC AAGGCCTCTG GGTATCCTTT CACAAACTAT 100
- GGAATGAACT GGGTGAAGCA GGCTCCAGGA CAGGGTTTAA AGTGGATGGG 150
- CTGGATTAAC ACCTCCACTG GAGAGTCAAC ATTTGCTGAT GACTTCAAGG 200
- SACGGTTTGA CTTCTCTTTG GAAACCTCTG CCAACACTGC CTATTTGCAG 250
- ATCAACAACC TCAAAAGTGA AGACATGGCT ACATATTTCT GTGCAAGATG 300
- GGAGGTTTAC CACGGCTACG TTCCTTACTG GGGCCAAGGG ACCACGGTCA 350
- CCGTCTCCTC A 361

SEQ ID NO:2

AACTAGA

5	MOLECULE ORIGINAL S IMMEDIATE	TYPE: nucleotid LENGTH: 407 b TYPE: plasmid OURCE ORGAN EXPERIMENT, ELL CLONE: pN	p DNA VISM: mouse AL SOURCE:	E. coli		
	FEATURES:	from 6 to 28 bp from 98 to 130 b from 176 to 196	pp (bp (MCK2 primer region CDR _{1L} CDR _{2L}	on	
15		from 293 to 319 from 374 to 404		CDR _{3L} MCK2 primer regio	ın	
	PROPERTIES FRP5			variable domain of		ibody
20						
	TCTAGTCACT	r ggatggtggg	AAGATGGAG	SA CATTGTGATG	ACCCAGTCTC	50
25	ACAAATTCCT	GTCCACTTCA	GTAGGAGAC	A GGGTCAGCAT	CACCTGCAAG	100
30	GCCAGTCAGG	ATGTGTATAA	TGCTGTTGC	C TGGTATCAAC	AGAAACCAGG	150
	ACAATCTCCT	AAACTTCTGA	TTTACTCGG	C ATCCTCCCGG	TACACTGGAG	200
35	TCCCTTCTCG	CTTCACTGGC	AGTGGCTCT	G GGCCGGATTT	CACTTTCACC	250

ATCAGCAGTG TGCAGGCTGA AGACCTGGCA GTTTATTTCT GTCAGCAACA 300

TTTTCGTACT CCATTCACGT TCGGCTCGGG GACAAAATTG GAAATAAAAC 350

GGGCTGATGC TGCACCAACT GTATCCATCT TCCCACCATC CAGTGACTAG 400

407

2

SEQ ID NO:3

	CEOURNOE TRADE
5	SEQUENCE TYPE: nucleotide
	SEQUENCE LENGTH: 175 bp
	MOLECULE TYPE: plasmid DNA
	ORIGINAL SOURCE ORGANISM: fully synthetic
	IMMEDIATE EXPERIMENTAL SOURCE: E. col
10	NAME OF CELL CLONE: pWW19
10	

	FEATURES:	from 30 to 35 bp from 38 to 44 bp		PstI site BstEII site for subcl variable domain	oning of heavy ch	ıain
15		from 54 to 98 bp		coding sequence of linker	(GlyGlyGlyGlyS	er) ₃
		from 105 to 110 from 112 to 117 from 120 to 125	bp	PvuII site BglII site BcII site for subclon	ing of light chain	variable
20			•	domain		
25	AAGCTTGCAT	GCAAGCTTCT	CAGGTACA	AC TGCAGGAGGT	CACCGTTTCC	50
20	TCTGGCGGTG	GCGGTTCTGG	TGGCGGTG	GC TCCGGCGGTG	GCGGTTCTGA	100
30	CATCCAGCTG	GAGATCTAGC	TGATCAAA	GC TCTAGAGGAT	CCCCGGGTAC	150
	CGAGCTCGAA	TTCACTGGCC	GTCGT			175

SEQ ID NO:4

SEQUENCE TYPE: nucleotide with corresponding protein SEQUENCE LENGTH: 748 bp MOLECULE TYPE: plasmid DNA ORIGINAL SOURCE CORGANISM: mouse IMMEDIATE EXPERIMENTAL SOURCE: E coli NAME OF CELL CLONE: pWW52 FEATURES: from 1 to 8 bp from 9 to 365 bp from 9 to 135 bp from 9 to 135 bp from 9 to 135 bp from 30 to 332 bp from 30 to 332 bp from 30 to 332 bp from 480 to 512 bp from 470 to 701 bp CDR _{1L} CDR _{2L} CDR _{3L} CDR _{3L} PROPERTIES: Fy heavy chain/light chain variable domain fusion protein binding to the extracellular domain of the growth factor receptor c-crbB-2 AAGCT TCT CAG GTA CAA CTG CAG CAG TCT GGA CCT GAA CTG Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu 5 10 AAG AAG CCT GGA GAG ACA GTC AAG ATC TCC TGC AAG GCC TCT Ser Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser 15 20 25 GGG TAT CCT TTC ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn Trp Val Lys Gln 30 35 40																
from 9 to 365 bp from 9 to 113 bp from 9 to 113 bp from 9 to 113 bp from 156 to 206 bp from 156 to 206 bp from 156 to 206 bp from 30 to 332 bp from 30 to 332 bp from 480 to 512 bp from 58 to 578 bp FRP5 light chain variable domain CDR1 from 58 to 578 bp CDR2 FROPERIES: Fv heavy chain/light chain variable domain fusion protein binding to the extracellular domain of the growth factor receptor c-erbB-2 AAGCT TCT CAG GTA CAA CTG CAG CAG TCT GGA CCT GAA CTG Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu 5 10 AAG AAG CCT GGA GAG ACA GTC AAG ATC TCC TGC AAG GCC TCT 83 Lys Lys Pro Gly Glu Thr Val Lys ILe Ser Cys Lys Ala Ser 15 20 25 GGG TAT CCT TTC ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn Trp Val Lys Gln 30 35 40 GCT CCA GGA CAG GGT TTA AAG TGG ATG GGC TGG ATT AAC ACT 167 Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr	5	MO ORI	LECU IGINA MEDI	JLE T VL SO ATE E	YPE: URCE XPE	H: 74 plasm E ORG RIME!	8 bp id DN ANIS NTAL	IA M: m	MICA		-	in				
CDR1L from 538 to 578 bp CDR1L from 575 to 701 bp CDR3L PROPERTIES: Fv heavy chain/light chain variable domain fusion protein binding to the extracellular domain of the growth factor receptor c-erbB-2 AAGCT TCT CAG GTA CAA CTG CAG CAG TCT GGA CCT GAA CTG Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu 5 10 AAG AAG CCT GGA GAG ACA GTC AAG ATC TCC TGC AAG GCC TCT 83 Lys Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser 15 20 25 GGG TAT CCT TTC ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG 125 Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn Trp Val Lys Gln 30 35 40 GCT CCA GGA CAG GGT TTA AAG TGG ATG GGC TGG ATT AAC ACT 167 Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr	15	FEA	ATUR	fi fi fi fi fi fi	rom 9 rom 9 rom 1 rom 30 rom 30 rom 4	to 365 9 to 11 56 to 2 03 to 3 66 to 4	5 bp 13 bp 206 bp 332 bp 110 bp 728 bo		F C C 1	RP5 h DR _{1H} DR _{2H} DR _{3H} 5 amin	eavy	chain ds linl	er sec	wence		
growth factor receptor c-crbB-2 AAGCT TCT CAG GTA CAA CTG CAG CAG TCT GGA CCT GAA CTG Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu 5 10 AAG AAG CCT GGA GAG ACA GTC AAG ATC TCC TGC AAG GCC TCT 83 Lys Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser 15 20 25 GGG TAT CCT TTC ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn Trp Val Lys Gln 30 35 40 GCT CCA GGA CAG GGT TTA AAG TGG ATG GGC TGG ATT AAC ACT 167 Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr	20			fi	rom 55	58 to 5	78 bp		c	DR _{1L} DR ₂			a.u.o.c	Goine		
Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu 5 10 AAG AAG CCT GGA GAG ACA GTC AAG ATC TCC TGC AAG GCC TCT 83 Lys Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser 15 20 25 GGG TAT CCT TTC ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG 125 Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn Trp Val Lys Gln 30 35 40 GCT CCA GGA CAG GGT TTA AAG TGG ATG GGC TGG ATT AAC ACT 167 Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr	25							ght ch	ain va	riable	domai	in fusi	on pro	otein b	inding	to the
AAG AAG CCT GGA GAG ACA GTC AAG ATC TCC TGC AAG GCC TCT Lys Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser 15 20 25 GGG TAT CCT TTC ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn Trp Val Lys Gln 30 35 40 GCT CCA GGA CAG GGT TTA AAG TGG ATG GGC TGG ATT AAC ACT Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr	30	AAG					ln L	eu G								41
Lys Lys Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser 15 20 25 GGG TAT CCT TTC ACA AAC TAT GGA ATG AAC TGG GTG AAG CAG Gly Tyr Pro Phe Thr Asn Tyr Gly Met Asn Trp Val Lys Gln 30 35 40 GCT CCA GGA CAG GGT TTA AAG TGG ATG GGC TGG ATT AAC ACT 167 Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr								5					10			
Gly Tyr Pro Phe Thr Asn Tyr Gly Met asn Trp Val Lys Gln 30 35 40 GCT CCA GGA CAG GGT TTA AAG TGG ATG GGC TGG ATT AAC ACT 167 Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr	35	AAG Lys	AAG Lys	Pro	GGA Gly	GAG Glu	ACA Thr	GTC Val	Lys	ATC Ile	TCC Ser	TGC Cys	AAG Lys	Ala	TCT Ser	83
GCT CCA GGA CAG GGT TTA AAG TGG ATG GGC TGG ATT AAC ACT 167 Ala Pro Gly Gln Gly Leu Lys Trp Met Gly Trp Ile Asn Thr	40				Phe					Met					Gln	125
	45	GCT Ala	CCA Pro	GGA Gly	CAG Gln	Gly	TTA Leu	AAG Lys	TGG Trp	ATG Met	Gly	TGG Trp	ATT Ile	AAC . Asn	ACT Thr	167

	TCC	ACT	GGA	GAG	TCA	ACA	TTT	GCT	GAT	GAC	TTC	AAG	GGA	CGG	209
	Ser	Thr	Gly	Glu	Ser	Thr	Phe	Ala	Asp	Asp	Phe	Lvs	Glv	Arg	
5	55					60				-	65		2		
	TTT	GAC	TTC	TCT	TTG	GAA	ACC	TCT	GCC	AAC	ACT	GCC	TAT	TTG	251
10	Phe	Asp	Phe	Ser	Leu	Glu	Thr	Ser	Ala	Asn	Thr	Ala	Tvr	Leu	231
		70					75					80		200	
	CAG	ATC	AAC	AAC	CTC	AAA	AGT	GAA	GAC	ATG	GCT	ACA	тат	TTC	293
15	Gln	Ile	Asn	Asn	Leu	Lys	Ser	Glu	Asp	Met	Ala	Thr	Tyr	Phe	2,5
			85					90	-				95		
	TGT	GCA	AGA	TGG	GAG	GTT	TAC	CAC	GGC	TAC	GTT	ССТ	TAC	TGG	335
20	Cys	Ala	Arg	Trp	Glu	Val	Tyr	His	Gly	Tyr	Val	Pro	Tvr	Tro	000
				100					105	-			-2-	110	
25	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTT	TCC	TCT	GGC	GGT	GGC	GGT	377
	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Glv	Glv	Glv	Glv	5.,
					115					120		2	011	013	
30	TCT	GGT	GGC	GGT	GGC	TCC	GGC	GGT	GGC	GGT	TCT	GAC	ATC	CAG	419
	Ser	${\tt Gly}$	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Asp	Ile	Gln	
	125					130					135	-			
35															
••	CTG	ACC	CAG	TCT	CAC	AAA	TTC	CTG	TCC	ACT	TCA	GTA	GGA	GAC	461
			Gln												
		140					145					150	-	-	
40															
	AGG	GTC	AGC	ATC	ACC	TGC	AAG	GCC	AGT	CAG	GAT	GTG	TAT	AAT	503
	Arg	Val	Ser	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val	Tyr	Asn	
			155					160					165		
45															
	GCT	GTT	GCC	TGG	TAT	CAA	CAG	AAA	CCA	GGA	CAA	TCT	ССТ	AAA	545
	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	
50				170					175					180	

	CTT	CTG	ATT	TAC	TCG	GCA	TCC	TCC	CGG	TAC	ACT	GGA	GTC	CCT	- 587
				Tyr											
5					185					190					
				ACT											629
10		Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Pro	Asp	Phe	Thr	Phe	
	195					200					205				
				AGT											671
15	Thr		Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr	Phe	
		210					215					220			
20				CAT											713
	Cys	Gln		His	Phe	Arg	Thr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	
			225					230					235		
25				GAG		TAGO	TGAT	CA A	AGCI	CTAC	SA.				748
	Thr	Lys	Leu	Glu	Ile										
				240											
30															

SEQ ID NO:	SEO	ID	NO:	5
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10	MO ORI IMN	LECU GINA (EDL	LE T L SO ATE E	PE: NGT: YPE: URCE XPER L CL	H: 22 plasm ORG	33 bp id DN IANIS VTAL	IA M: m SOUI	ouee s	nd F	coli	in							
15	FEATURES: from 1 to 22 bp from 23 to 85 bp from 89 to 445 bp trom 446 to 490 bp from 491 to 814 bp from 815 to 2155 bp from 2156 to 2233 bp								ompA 5' non-coding region ompA signal peptide FRPS heavy chain variable domain 15 amino acids linker sequence FRPS light chain variable domain coding region of phoA 3' non-coding region of phoA									
20	PRO fusio	PERT on pro	IES: tein F	Fv he v(FRP	avy cł 5)-pho	ain/lig A bin	ght cha	ain var o the g	riable growti	domai 1 facto	n and	alkali ptor c	ne pho erbB-	osphata 2	ıse			
25	TCT	AGAT.	AAC	GAGG	CGCA	AA A	A	ATG	AAA	AAG	ACA	GCT	ATC	GCG	43			
								Met	Lys	Lys	Thr	Ala	Ile	Ala				
									-20					-15				
30	ATT	GCA	GTG	GCA	CTG	GCT	GGT	TTC	GCT	ACC	GTA	GCG	CAA	GCT	85			
												Ala			05			
					-10		-			-5			0111	1114				
35										•								
30	TCT	CAG	GTA	CAA	CTG	CAG	CAG	TCT	GGA	ССТ	GAA	CTG	DAG	AAG	127			
												Leu						
	1					5			-		10		-,-	-30				
40																		
	CCT	GGA	GAG	ACA	GTC	AAG	ATC	TCC	TGC	AAG	GCC	TCT	GGG	TAT	169			
												Ser						
45	15					20					25		_					
	CCT	TTC	ACA	AAC	TAT	GGA	ATG	AAC	TGG	GTG	AAG	CAG	GCT	CCA	211			
												Gln			,			
50		30					35				-	40						

	GGA	CAG	GGT	TTA	AAG	TGG	ATG	GGC	TGG	ATT	AAC	ACC	TCC	ACT	253
5	Gly	Gln	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Ser	Thr	
			45					50					55		
10													TTT		295
10	Gly	Glu	Ser		Phe	Ala	Asp	Asp	Phe	Lys	Gly	Arg	Phe	Asp	
				60					65					70	
	mmo	mom													
15													CAG		337
	rne	ser	ьeu	GIU	75	ser	Ата	Asn	Thr		lyr	Leu	Gln	Ile	
					75					80					
20	AAC	AAC	CTC	AAA	AGT	GAA	GAC	ATG	GCT	ACA	тат	TTC	TGT	GCA	379
													Cys		
	85					90					95		-		
25	AGA	TGG	GAG	GTT	TAC	CAC	GGC	TAC	GTT	CCT	TAC	TGG	GGC	CAA	421
	Arg		Glu	Val	Tyr	His	Gly	Tyr	Val	Pro	Tyr	Trp	Gly	Gln	
		100					105					110			
30															
													TCT		463
	GIY	Thr		Val	Thr	Val	Ser		Gly	Gly	Gly	Gly	Ser	Gly	
			115					120					125		
35	GGC	ССТ	ccc	TICC	ccc	ccm	000	oom.	mom		1 ma	~1.0	CTG		
													Leu		505
	017	013	CLY	130	GLY	GLY	Gry	GIY	135	мар	TIE	GIII	rea	140	
40									133					140	
	CAG	TCT	CAC	AAA	TTC	CTG	TCC	ACT	TCA	GTA	GGA	GAC	AGG	GTC	547
													Arg		
45					145					150					
													GCT		589
		Ile	Thr	Cys	Lys		Ser	Gln	Asp	Val	Tyr	Asn	Ala	Val	
50	155					160					165				

	GCC	TGG	TAT	CAA	CAG	AAA	CCA	GGA	CAA	TCT	CCI	AAA	CTI	CTG	631
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5		170					175					180			
												100			
	ATT	TAC	TCG	GCA	TCC	TCC	CGG	TAC	ACT	CCA	CTC	CCT	mem	CGC	673
10	Ile	Tvr	Ser	Ala	Ser	Ser	Ara	The	Mbw	01	. 77-1	CCI	TCT	Arg	673
		-	185			-	9	190		GIY	val	PIO		Arg	
			100					190					195		
	THE	A CT	ccc	» Cm	ccc	mom	-							,	
15	Pho	The	GGC	AG1	GGC	TCT	GGG	CCG	GAT	TTC	ACT	TTC	ACC	ATC	715
	- ***	1111	Gly	200	GIY	ser	GIY	Pro		Phe	Thr	Phe	Thr	Ile	
				200					205					210	
	100	3.0m	ama												
20			GTG												757
	ser	ser	Val	GIn		Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	
					215					220					
25	CAA	CAT	TTT	CGT	ACT	CCA	TTC	ACG	TTC	GGC	TCG	GGG	ACA	AAA	799
	Gln	His	Phe	Arg	Thr	Pro	Phe	Thr	Phe	Gly	Ser	Gly	Thr	Lys	
	225					230					235				
30	TTG	GAG	ATC	AAA	GCT	CTA	GAG	CCT	GTT	CTG	GAA	AAC	CGG	GCT	841
	Leu	Glu	Ile	Lys	Ala	Leu	Glu	Pro	Val	Leu	Glu	Asn	Ara	Ala	
		240					245					250	5		
35															
••	GCT	CAG	GGC	GAT	ATT	ACT	GCA	ccc	GGC	GGT	CCT	ccc	COT	TTTA	883
			Gly												553
			255	-				260	01)	GLY	ALG	MIG	-	ren	
40								200					265		
	ACG	GGT	GAT	CAG	аст	ccc	CCT	CTTC	ccm	C a m	mam				
	Thr	Glv	Asp	Gln	Thr	Ala	Ala	LOU	700	GAT	C	CTT	AGC	GAT	925
		2		270		nia	nia	Leu		Asp	ser	ьeи	Ser		
45				270					275					280	
	222	ССТ	CCA	222	220	3 mm	3 mm								
			GCA												967
	шys	LT.O	Ala			тте	тте	ren			Gly	Asp	Gly	Met	
50					285					290					

	GGG	GAC	TCG	GAA	ATT	ACT	GCC	GCA	CGT	AAT	TAT	GCC	GAA	GGT	1009
	Gly	Asp	Ser	Glu	Ile	Thr	Ala	Ala	Arg	Asn	Tyr	Ala	Glu	Gly	
5	295					300					305			•	
	GCG	GGC	GGC	TTT	TTT	AAA	GGT	ATA	GAT	GCC	тта	CCG	CTT	ACC	1051
			Gly												1031
10		310	_			-	315					320	Dea	1111	
												320			
	GGG	CAA	TAC	АСТ	CAC	тат	ccc	CTC	አአጥ	222	222	300	000		1093
15			Tyr												1093
			325			-1-	,,,,,	330	non	БуS	цуь	1111		Lys	
								330					335		
	CCG	GAC	TAC	GTC	ACC	GAC	TCG	CCT	CCA	mc a	CCA	3.00	000	maa	1135
20			Tyr												1135
			-2 -	340	••••		561	7120	345	Ser	AIG	TIII	MIA	~	
									343					350	
25	TCA	ACC	GGT	GTC	444	ACC	ጥለጥ	220	ccc	ccc	cmc	000	ото	GAT	1100
20			Gly												1177
			023	141	355	1111	TYT	Maii	GIY	360	reu	GIY	vai	Asp	
					333					300					
30	АТТ	CAC	GAA	444	CAT	CAC	CCA	300	a mm	cma	C3.3	3.000			1010
			Glu												1219
	365	111.5	GIU	пуъ	мър	370	PIO	mr	iie	Leu		Met	Ala	Lys	
	505					3/0					375				
35	ccc	CCA	ccm	Omo	000								- 30		
			GGT												1261
	MIA		Gly	Leu	Ala	ınr		Asn	Val	Ser	Thr		Glu	Leu	
40		380					385					390			
	010		-												
			GCC												1303
	GIII	Asp	Ala	ınr	Pro	Ala	Ala		Val	Ala	His	Val		Ser	
45			395					400					405		
			TGC												1345
	Arg	Lys	Суз		Gly	Pro	Ser	Ala		Ser	Glu	Lys	Cys	Pro	
50				410					415					420	

	GGT	AAC	GCT	CTG	GAA	AAA	GGC	GGA	AAA	GGA	TCG	ATT	ACC	GAA	1387
_	Gly	Asn	Ala	Leu	Glu	Lys	Gly	Gly	Lys	Gly	Ser	Ile	Thr	Glu	
5					425					430					
			CTT												1429
10		Leu	Leu	Asn	Ala		Ala	Asp	Val	Thr	Leu	Gly	Gly	Gly	
	435					440					445				
	GC A	222	ACC	TTTT	CCT	CAA	200	003	200	COM	00m				
15			Thr												1471
		450		*****		oru	455	niu	****	nia	GLY	460	пр	GIII	
							133				,	400			
20	GGA	AAA	ACG	CTG	CGT	GAA	CAG	GCA	CAG	GCG	CGT	GGT	TAT	CAG	1513
	Gly	Lys	Thr	Leu	Arg	Glu	Gln	Ala	Gln	Ala	Arg	Gly	Tyr	Gln	
			465					470					475		
25	TTG	GTG	AGC	GAT	GCT	GCC	TCA	CTG	AAT	TCG	GTG	ACG	GAA	GCG	1555
	Leu	Val	Ser	Asp	Ala	Ala	Ser	Leu	Asn	Ser	Val	Thr	Glu	Ala	
				480					485					490	
30															,
														AAT	1597
	Asn	Gln	Gln	Lys		Leu	Leu	Gly	Leu	Phe	Ala	Asp	Gly	Asn	
					495					500					
35	1 mc	003	omo		maa					2					
			GTG												1639
	505	FIO	Val	Arg	пр	510	GIY	Pro	ьуs	АТА		Tyr	His	GLy	
40	505					210					515				
	AAT	ATC	GAT	AAG	ccc	GCA	GTC	ACC	TGT	ACG	CCA	таа	CCG	('AA	1681
			Asp												1001
45		520					525					530		•	
	CGT	AAT	GAC	AGT	GTA	CCA	ACC	CTG	GCG	CAG	ATG	ACC	GAC	AAA	1723
			200	a	** . *	D	mh~	T 0	27.0	01-	35-6				
	Arg	ASII	мър	ser	vaı	Pro	1111	ьец	Ald	GIII	Mec	Thr	ASD	Lys	
50	Arg	ASII	535	ser	vaı	PIO	1111	540	міа	GIII	Mec	Thr	545	Lys	
50	Arg	ASII		ser	vaı	PTO	1111		Ald	GIII	mec	Thr		Lys	

GCC	ATT	GAA	TTG	TTG	AGT	AAA	AAT	GAG	AAA	GGC	TTT	TTC	CTG	1765
Ala	Ile	Glu	Leu	Leu	Ser	Lys	Asn	Glu	Lys	Gly	Phe	Phe	Leu	
			550							_				
													200	
CAA	GTT	GAA	GGT	GCG	TCA	ATC	GAT	AAA	CAG	CAT	Cam	CCT	ccc	1807
														1007
							LLOP	2,5		nap	nis	Ала	MIG	
									5,0					
AAT	ССТ	TGT	GGG	CAA	יויינימ	GGC	GAC	NCC.	cmc	Cam	omo			
														1849
		-20	013	OIII		GLY	GIU	1111	vai		Leu	Asp	Glu	
3.3					300					585				
GCC	СПР	CAA	ccc	ccc	CIDC	CAA	mmo	com			~-~			
														1891
		01	ura	ALG	neu		Pile	Ala	ьys	ьуs		GIY	Asn	
	550					232					600			
NCC.	СТС	CTC	a ma	ama	100		~							
														1933
THE	теп		TIE	val	Thr	Ala		His	Ala	His	Ala		Gln	
		605					610					615		
3 mm	-													
														1975
TIE	Val	Ala		Asp	Thr	Lys	Ala	Pro	Gly	Leu	Thr	Gln	Ala	
			620					625					630	
														2017
Leu	Asn	Thr	Lys	Asp	Gly	Ala	Val	Met	Val	Met	Ser	Tyr	Gly	
				635					640					
														2059
Asn	Ser	Glu	Glu	Asp	Ser	Gln	Glu	His	Thr	Gly	Ser	Gln	Leu	
645					650					655				
CGT	ATT	GCG	GCG	TAT	GGC	CCG	CAT	GCC	GCC	AAT	GTT	GTT	GGA	2101
	660					665					670			
	AACG Thr ATT Ile CTA Leu AAC CST CGT CGT CGT CGT CAACA CGT	AAT CCT ASN PTO 575 GCC GTA Ala Val 590 ACG CTG Thr Leu ATT GTT Ile Val CTA AAT Leu ASN AAC TCC ASN Ser 645 CGT ATT Arg Ile	ALA ILE GLU CAA GTT GAA GIN VAI GLU AAT CCT TGT ASN Pro Cys 575 GCC GTA CAA ALA VAI GIN 590 ACG CTG GTC Thr Leu VAI 605 ATT GTT GCG ILE VAI ALA CTA AAT ACC Leu ASN Thr AAC TCC GAA ASN Ser Glu 645 CGT ATT GCG ATT GC	Ala Ile Glu Leu 550 CAA GTT GAA GGT Gln Val Glu Gly AAT CCT TGT GGG Asn Pro Cys Gly 575 GCC GTA CAA CGG Ala Val Gln Arg 590 ACG CTG GTC ATA Thr Leu Val Ile 605 ATT GTT GCG CCG Ile Val Ala Pro 620 CTA AAT ACC AAA Leu Asn Thr Lys AAC TCC GAA GAG Asn Ser Glu Glu 645 CGT ATT GCG GCG Arg Ile Ala Ala	Ala Ile Glu Leu Leu 550 CAA GTT GAA GGT GCG Gln Val Glu Gly Ala 565 AAT CCT TGT GGG CAA Asn Pro Cys Gly Gln 575 GCC GTA CAA CGG GCG Ala Val Gln Arg Ala 590 ACG CTG GTC ATA GTC Thr Leu Val Ile Val 605 ATT GTT GCG CCG GAT Ile Val Ala Pro Asp 620 CTA AAT ACC AAA GAT Leu Asn Thr Lys Asp 635 AAC TCC GAA GAG GAT Asn Ser Glu Glu Asp 645 CGT ATT GCG GCG TAT Arg Ile Ala Ala Tyr	ALA ILE GIU LEU LEU SER 550 CAA GTT GAA GGT GCG TCA GIN VAI GIU GIY ALA SER 565 AAT CCT TGT GGG CAA ATT Asn Pro Cys GIY GIN ILE 575 GCC GTA CAA CGG GCG CTG ALA VAI GIN ATG ALA LEU 590 ACG CTG GTC ATA GTC ACC THr LEU VAI ILE VAI THR 605 ATT GTT GCG CCG GAT ACC ILE VAI ALA Pro Asp Thr 620 CTA AAT ACC AAA GAT GGC LEU ASN THR LYS Asp GIY 635 AAC TCC GAA GAG GAT TCA Asn Ser Glu Glu Asp Ser 645 CGT ATT GCG GCG TAT GGC ATG ILE VAI ALA ALA TAC GAT GGC CGG ATT GGC ATG ILE ALA ALA TYR GIY	Ala Ile Glu Leu Leu Ser Lys 550 CAA GTT GAA GGT GCG TCA ATC Gln Val Glu Gly Ala Ser Ile 565 AAT CCT TGT GGG CAA ATT GGC Asn Pro Cys Gly Gln Ile Gly 575 GCC GTA CAA CGG GCG CTG GAA Ala Val Gln Arg Ala Leu Glu 590 ACG CTG GTC ATA GTC ACC GCT Thr Leu Val Ile Val Thr Ala 605 ATT GTT GCG CCG GAT ACC AAA Ile Val Ala Pro Asp Thr Lys 620 CTA AAT ACC AAA GAT GGC GCA Leu Asn Thr Lys Asp Gly Ala 635 AAC TCC GAA GAG GAT TCA CAA Asn Ser Glu Glu Asp Ser Gln 645 CGT ATT GCG GCG TAT GGC CCG Arg Ile Ala Ala Tyr Gly Pro	ALA ILE GLU LEU LEU SER LYS ASN 550 CAA GTT GAA GGT GCG TCA ATC GAT Gln Val Glu Gly Ala Ser Ile Asp 565 AAT CCT TGT GGG CAA ATT GGC GAG Asn Pro Cys Gly Gln ILE Gly Glu 575 GCC GTA CAA CGG GCG CTG GAA TTC Ala Val Gln Arg Ala Leu Glu Phe 590 ACG CTG GTC ATA GTC ACC GCT GAT Thr Leu Val Ile Val Thr Ala Asp 605 ATT GTT GCG CCG GAT ACC AAA GCT Ile Val Ala Pro Asp Thr Lys Ala 620 CTA AAT ACC AAA GAT GGC GCA GTG Leu Asn Thr Lys Asp Gly Ala Val 635 AAC TCC GAA GAG GAT TCA CAA GAA Asn Ser Glu Glu Asp Ser Gln Glu 645 CGT ATT GCG GCG TAT GGC CCG CAT Arg ILE Ala Ala Tyr GGV PTO His	Ala Ile Glu Leu Leu Ser Lys Asn Glu 550 CAA GTT GAA GGT GCG TCA ATC GAT AAA Gln Val Glu Gly Ala Ser Ile Asp Lys 565 AAT CCT TGT GGG CAA ATT GGC GAG ACG Asn Pro Cys Gly Gln Ile Gly Glu Thr 575 GCC GTA CAA CGG GCG CTG GAA TTC GCT Ala Val Gln Arg Ala Leu Glu Phe Ala 590 ACG CTG GTC ATA GTC ACC GCT GAT CAC Thr Leu Val Ile Val Thr Ala Asp His 605 ATT GTT GCG CCG GAT ACC AAA GCT CCG Ile Val Ala Pro Asp Thr Lys Ala Pro 620 CTA AAT ACC AAA GAT GGC GCA GTG ATG Leu Asn Thr Lys Asp Gly Ala Val Met 635 AAC TCC GAA GAG GAT TCA CAA GAA CAT Asn Ser Glu Glu Asp Ser Gln Glu His 645 CGT ATT GCG GCG TAT GGC CCG CAT GCC Arg Ile Ala Ala Tyr Gly Pro His Ala	ALA ILE GLU LEU LEU SER LYS ASN GLU LYS 555 CAA GTT GAA GGT GCG TCA ATC GAT AAA CAG GLN VAI GLU GLY ALA SER ILE ASP LYS GLN 565 AAT CCT TGT GGG CAA ATT GGC GAG ACG GTC ASN Pro Cys Gly Gln ILE GLY GLU THr VAI 575 GCC GTA CAA CGG GCG CTG GAA TTC GCT AAA ALA VAI GLN Arg Ala Leu Glu Phe Ala Lys 590 ACG CTG GTC ATA GTC ACC GCT GAT CAC GCC THr Leu Val ILE Val Thr Ala Asp His Ala 610 ATT GTT GCG CCG GAT ACC AAA GCT CCG GGC ILE VAI ALA Pro Asp Thr Lys Ala Pro Gly 620 CTA AAT ACC AAA GAT GGC GCA GTG ATG GTG CCG GAC GCC GAT GCC GCC GTG ATT GCC GCC GAT GCC GCC GCT ATT GCG GCC GCC GCC GCC GCC GCC GCC GCC G	ALA ILE GLU LEU LEU SER LYS ASN GLU LYS GLY 5550 CAA GTT GAA GGT GCG TCA ATC GAT AAA CAG GAT GAN VAI GLU GLY ALA SER ILE ASP LYS GLN ASP 565 AAAT CCT TGT GGG CAA ATT GGC GAG ACG GTC GAT ASN Pro Cys Gly Gln ILE GLY GLU THY VAI ASP 575 AAAT CCT TGT GGG CAG ATT GGC GAG ACG GTC GAT ASN Pro Cys Gly Gln ILE GLY GLU THY VAI ASP 585 GCC GTA CAA CGG GCG CTG GAA TTC GCT AAA AAG ALA VAI Gln Arg Ala Leu Glu Phe Ala Lys Lys 590 ACG CTG GTC ATA GTC ACC GCT GAT CAC GCC CAC THY Leu VAI ILE VAI THY ALA ASP HIS ALA HIS 605 ATT GTT GCG CCG GAT ACC AAA GCT CCG GGC CTC ILE VAI ALA Pro ASP THY LYS ALA PRO GLY Leu ASN THY LYS ASP GLY ALA VAI MET VAI MET 635 CTA AAT ACC AAA GAT GCC GCA GTG ATG GTG ATG CAC GAC ASN SEY GLU GLU ASP SEY GLN GLU HIS THY GLY 645 AAC TCC GAA GAG GAT TCA CAA GAA CAT ACC GGC ASN SEY GLU GLU ASP SEY GLN GLU HIS THY GLY 645 CGT ATT GCG GCG TAT GGC CCG CAT GCC GCC AAT ACR GCG TATT GCG GCG GCT ATT GCG GCC AAT ACT GCC GCC GCC AAT ACT GCC GCC AAT ACT GCC GCC GCC AAT ACT GCC GCC GCC AAT ACT GCC GCC AAT ACT GCC GCC AAT ACT GCC GCC GCC GCC GCC GCC GCC GCC GCC G	Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe 555 555 CAA GTT GAA GGT GCG TCA ATC GAT AAA CAG GAT CAT GIN Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His 565 570 585 570 AAT CCT TGT GGG CAA ATT GGC GAG ACG GTC GAT CTC Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu 575 580 585 GCC GTA CAA CGG GCG CTG GAA TTC GCT AAA AAG GAG Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu 590 595 600 ACG CTG GTC ATA GTC ACC GCT GAT CAC GCC CAC GCC Thr Leu Val Ile Val Thr Ala Asp His Ala His Ala 605 610 ATT GTT GCG CCG GAT ACC AAA GCT CCG GGC CTC ACC Ile Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr 620 625 CTA AAT ACC AAA GAT GGC GCA GTG ATG GTG ATG AGT Leu Asn Thr Lys Asp Gly Ala Val Met Val Met Ser 635 640 AAC TCC GAA GAG GAT TCA CAA GAA CAT ACC GGC AGT ASN Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser 645 650 655 CGT ATT GCG CGG CTAT GCC CCG CAT GCC CAA ATG TTA ATT GCG CGC GCT TAT GCC CCC CAAT GTT ATG ILE Ala Ala Ala Tyr Gly Pro His Ala Ala Asn Val	Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe 5550 CAA GTT GAA GGT GCG TCA ATC GAT AAA CAG GAT CAT GCT Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala 5655 AAT CCT TGT GGG CAA ATT GGC GAG ACG GTC GAT CTC GAT Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp 575 GCC GTA CAA CGG GCG CTG GAA TTC GCT AAA AAG GAG GGT Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly 590 ACG CTG GTC ATA GTC ACC GCT GAT CAC GCC ACC GCC ACC GCT AT GCT GTT GCG GCC AT GCT GAT ASA AAG GAG GTT GAT GTT GCG CCG GAT ACC AAA GCT CCG GGC CTC ACC ACC GCT AT GCT GCT AAA AAG GCT CCG GCC ACC GCA ACC GCT ACC ACC ACC GCT ACC ACC GCT ACC ACC ACC ACC ACC ACC ACC ACC ACC A	CAA GTT GAA GGT GCG TCA ATC GAT AAA CAG GAT CAT GCT GCG Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala 565 570 AAT CCT TGT GGG CAA ATT GGC GAG ACG GTC GAT CTC GAT GAA Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu 575 580 585 GCC GTA CAA CGG GCG CTG GAA TTC GCT AAA AAG GAG GGT AAC Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn 590 595 600 ACG CTG GTC ATA GTC ACC GCT GAT CAC GCC CAC GCC AGC CAG Thr Leu Val Ile Val Thr Ala Asp His Ala His Ala Ser Gln 605 610 610 ATT GTT GCG CCG GAT ACC AAA GCT CCG GGC CTC ACC CAG GCG Ile Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala 620 625 630 CTA AAT ACC AAA GAT GGC GCA GTG ATG GTG ATG AGT TAC GGG Leu Asn Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly 635 640 AAC TCC GAA GAG GAT TCA CAA GAA CAT ACC GGC AGT CAG TTG Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu 645 650 655 CGT ATT GCG GCG TAT GCC CCG CAT GCC GCA AAT GTT GTT GGA Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly

GCT 2143
Ala
2185
2233

SEQ ID NO:6

SEQUENCE TYPE: nucleotide

•	SEQUENCE	LENGTH: 342 bp				
	MOLECULE	TYPE: plasmid I	ONA			
	ORIGINAL S	OURCE ORGAN	IISM: mouse			
10	IMMEDIATE	EXPERIMENT	AL SOURCE:	E.coli		
	NAME OF C	ELL CLONE: pW	W15-VH51-1			
15	FEATURES:	from 1 to 14 bp	pa	rtial sequence of	VH1BACK primer	r region
		from 82 to 96 bp		OR _{IH}		
		from 139 to 189		OR _{2H}		
		from 286 to 318	bp CI	OR _{3H}		
20		from 317 to 342	bp pa	rtial sequence of	VH1FOR primer r	egion
	PROPERTIES	S: encodes the hea	vy chain varia	ble domain of mo	noclonal antibody	FWP5
25					•	
	CTGCAGCAG	r ctggggctga	GCTGGTGAG	G CCTGGGACT	I CAGTGAAGCT	50
30	GTCCTGCAA	GCTTCTGATT	ACACCTTCA	C CAGCTACTG	G ATGAACTGGG	100
	TGAAGCAGAG	GCCTGGACAA	GGCCTTGAZ	T GGATTGGTA	r gattgatcct	150
35						
	TCAGACAGTO	AAACTCAATA	CAATCAAAT	G TTCAAGGAC	A AGGCCGCATT	200
	GACTGTAGAC	AAGTCCTCCA	ATACAGCCT	A CATGCAACTO	AGCAGCCTGA	250
40						
	CATCTGAGG	CTCTGCGGTC	TATTACTGT	G CAAAAGGGGG	GGCCTCTGGG	300

342

GACTGGTACT TCGATGTCTG GGGCCAAGGG ACCACGGTCA CC

SEQ ID NO:7

5	SEQUENCE TYPE: nucleotide SEQUENCE LENGTH: 310 bp								
		TYPE: plasmid D							
40		OURCE ORGAN							
10		EXPERIMENTA			coli				
	NAME OF CE	ELL CLONE: pW	W15-VL5	1-1					
15	FEATURES:	from 1 to 18 bp				/K1BACK primer	region		
		from 64 to 96 bp		CDR					
		from 142 to 162	•	CDR					
20		from 259 to 282	•	CDR					
		from 292 to 310	ор	partia	al sequence of V	/K1FOR primer re	egion		
25	PROPERTIES	: encodes the ligh	ıt chain var	iable	domain of mone	oclonal antibody F	WP51		
20									
	CAGCTGACCC	AGTCTCCATC	CTCACTG	STCT	GCATCTCTGG	GAGGCGAAGT	50		
30	CACCATCACT	TGCAAGGCAA	GCCAAGA	CAT	TAAGAAGTAT	ATAGCTTGGT	100		
35	ACCAACACAA	GCCTGGAAAA	AGTCCTC	GGC	TACTCATACA	CTACACATCT	150		
	GTATTACAGC	CAGGCATCCC	ATCCAGG	TTC	AGTGGAAGTG	GGTCTGGGAG	200		
40	AGATTATTCC	TTCAGCATCC	ACAACCT	GGA	GCCTGAAGAT	ATTGCAACTT	250		
	ATTATTGTCT	ACATTATGAT	TATCTGT	'ACA	CGTTCGGAGG	GGGCACCAAG	300		
45	CTGGAGATCT						310		

SEO	ID	NO	٠.8

35

SEQUENCE TYPE: nucleotide with corresponding protein SEQUENCE LENGTH: 748 bp MOLECULE TYPE: plasmid DNA ORIGINAL SOURCE ORGANISM: mouse IMMEDIATE EXPERIMENTAL SOURCE: E.coli

NAME OF CELL CLONE; pWW15-Fv51

15	FEATURES:	from 1 to 8 bp	synthetic spacer
		from 9 to 368 bp	FWP 51 heavy chain variable domain
		from 99 to 113 bp	CDR1H
20		from 156 to 206 bp	CDR2H
		from 303 to 335 bp	CDR3H
		from 369 to 413 bp	synthetic spacer
		from 414 to 728 bp	FWP 51 light chain variable domain
25		from 483 to 515 bp	CDR1L
		from 561 to 581 bp	R2L
		from 678 to 701 bp	CDR3L
30		from 729 to 748 bp	synthetic spacer

PROPERTIES: encodes single-chain Fv fusion gene comprising monoclonal antibody FWP51 heavy and kappa light chain variable domain cDNA

AAGCT 5

TCT CAG GTA CAA CTG CAG CAG TCT GGG GCT GAG CTG GTG
Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val
1 5 10

AGG CCT GGG ACT TCA GTG AAG CTG TCC TGC AAG GCT TCT GAT AAG PPO Gly Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Asp
15 20 25

	TAC	ACC	TTC	ACC	AGC	TAC	TGG	ATG	AAC	TGG	GTG	AAG	CAG	AGG	128
	Tyr	Thr	Phe	Thr	Ser	Tyr	Trp	Met	Asn	Trp	Va1	Lys	Gln	Arg	
5			30					35					40		
	CCT	GGA	CAA	GGC	CTT	GAA	TGG	ATT	GGT	ATG	ATT	GAT	CCT	TCA	170
10	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Met	Ile	Asp	Pro	Ser	
				45					50					55	
			GAA												212
15	Asp	Ser	Glu	Thr		Tyr	Asn	Gln	Met	Phe	Lys	Asp	Lys	Ala	
					60					65					
20			ACT												254
		Leu	Thr	Val	Asp		Ser	Ser	Asn	Thr	Ala	Tyr	Met	Gln	
	70					75					80				
25			AGC												296
	Leu		Ser	Leu	Thr	Ser		Asp	Ser	Ala	Val	Tyr	Tyr	Cys	
		85					90					95			
30															
			GGG												338
	AIA	цуs	Gly	GIY	Ala	Ser	Gly		Trp	Tyr	Phe	Asp		Trp	
35			100					105					110		
30	ccc	CAA	000	100	100	oma									
			GGG												380
	GIĀ	GIII	Gly	115	Thr	vaı	unr	vaı		Ser	GIĀ	Gly	Gly	-	
40				115					120					125	
	тст	GGT	GGC	GGT	GGC	TICC	ccc	CCT	ccc	ССШ	mcm	030	3.000	010	400
			Gly												422
45	DCI	CLY	Ory	GLY	130	ber	GIY	GIĀ	GIY	135	ser	Asp	ше	GIN	
					-50					133					
	CTG	ACC	CAG	ጥርጥ	CCA	TCC	тсъ	CTC	TICT.	GCA	mcm	CTTC	CCI	ccc	161
			Gln												464
50	_ 50				0	145	551	_cu	DCL		150	пец	GTA	GTÅ	

	GAA	GTC	ACC	ATC	ACT	TGC	AAG	GCA	AGC	CAA	GAC	ATT	AAG	λAG	506
														Lys	
5		155					160					165	-,, -	270	100
	TAT	ATA	GCT	TGG	TAC	CAA	CAC	AAG	CCT	GGA	AAA	AGT	CCT	CGG	548
10					Tyr										182
			170					175					180		
	CTA	CTC	ATA	CAC	TAC	ACA	TCT	GTA	TTA	CAG	CCA	GGC	ATC	CCA	590
15					Tyr										
				185					190					195	
20	TCC	AGG	TTC	AGT	GGA	AGT	GGG	TCT	GGG	AGA	GAT	TAT	TCC	TTC	632
	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Arg	Asp	Tyr	Ser	Phe	
					200					205					
25					CTG										674
		Ile	His	Asn	Leu	Glu	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	
	210					215					220				
30															
					GAT										716
	Cys		His	Tyr	Asp	Tyr	Leu	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	
35		225					230					235			
30															
	AAG				TAGO	TGAT	CA A	AGCI	CTAG	A					748
	Lys	Leu		Ile											
40			240												

CEO	ID	NO:9
SEU	w	NO.9

5	SEQUENCE TYPE: nucleotide
	SEQUENCE LENGTH: 201 bp
	MOLECULE TYPE: plasmid DNA
	ORIGINAL SOURCE ORGANISM: Pseudomonas aeruginosa PAK
10	IMMEDIATE EXPERIMENTAL SOURCE: E.coli
	NAME OF CELL CLONE: pWW22

15 20	FEATURES:	from 1 to 27 bp from 29 to 201 b	•	partia nucle exoto	otide positions	quence correspond 1574 to 1747 bp o (Gray et al., Proc. 1645, 1984)	f the
25	PROPERTIES aeruginosa PA	: encodes part of K	the mutated	d exot	oxin A gene from	n <u>Pseudomonas</u>	
	AAGCTTAAGG	G AGATCTGCAT	GCTTCTA	GAG	GGCGGCAGCC	TGGCCGCGCT	50
30	GACCGCGCAC	CAGGCCTGCC	ACCTGCC	GCT	GGAGACTTTC	ACCCGTCATC	100
	GCCAGCCGCG	GGGCTGGGAA	CAACTGG	AGC	AGTGCGGCTA	TCCGGTGCAG	150
35	CGGCTGGTCG	CCCTCTACCT	GGCGGCG	CGA	CTGTCATGGA	ACCAGGTCGA	200

SEQ ID NO:10

35

5	SEQUENCE TYPE: nucleotide with corresponding protein
	SEQUENCE LENGTH: 2012 bp
	MOLECULE TYPE: plasmid DNA
10	ORIGINAL SOURCE ORGANISM: mouse/P.acruginosa
	IMMEDIATE EXPERIMENTAL SOURCE: E.coli
	NAME OF CELL CLONE: pWW215-5

15	FEATURES:	from 1 to 63 bp	ompA signal peptide
		from 64 to 87 bp	FLAG peptide and enterokinase cleavage
		C	site
20		from 97 to 453 bp	FRP5 heavy chain variable domain
		from 454 to 498 bp	15 amino acids linker sequence
		from 499 to 822 bp	FRP5 light chain variable domain
		from 826 to 1911 bp	exotoxin A gene coding region
25			(coding for amino acids 252 to 613 of the mature exotoxin A)
		from 1912 to 2012 bp	3'non-coding region of the exotoxin A
30			gene

PROPERTIES: Fv heavy chain/light chain variable domain and exotoxin A fusion protein Fv(FRP5)-ETA binding to the c-erbB-2 protein

ATG AAA AAG ACA GCT ATC GCG ATT GCA GTG GCA CTG GCT GGT 42

Met Lys Lys Thr Ala 1le Ala 1le Ala Val Ala Leu Ala Gly

-30

-25

-20

TTC GCT ACC GTT GCG CAA GCT GAC TAC AAG GAC GAC GAT GAC 84

Phe Ala Thr Val Ala Gln Ala Asp Tyr Lys Asp Asp Asp Asp

-15

-10

-5

AAG CTA GCT TCT CAG GTA CAA CTG CAG CAG TCT GGA CCT GAA 126
Lys Leu Ala Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu

1 5 10

	CTG	AAG	AAG	CCT	GGA	GAG	ACA	GTC	AAG	ATC	TCC	TGC	AAG	GCC	168
	Leu	Lys	Lys	Pro	Gly	Glu	Thr	Va1	Lys	Ile	Ser	Cys	Lys	Ala	
5	•			15					20					25	
	TCT	GGG	TAT	CCT	TTC	ACA	AAC	TAT	GGA	ATG	AAC	TGG	GTG	AAG	210
10	Ser	Gly	Tyr	Pro	Phe	Thr	Asn	Tyr	Gly	Met	Asn	Trp	Val	Lys	
					30					35					
														AAC	252
15	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Lys	Trp	Met	Gly	Trp	Ile	Asn	
	40					45					50				
20														GGA	294
	Thr		Thr	Gly	Glu	Ser	Thr	Phe	Ala	Asp	Asp	Phe	Lys	Gly	
		55					60					65			
25									TCT						336
	Arg	Phe		Phe	Ser	Leu	Glu	Thr	Ser	Ala	Asn	Thr	Ala	Tyr	
			70					75					80		
30															
									GAA						378
	Leu	GIn	Ile		Asn	Leu	Lys	Ser	Glu	Asp	Met	Ala	Thr	Tyr	
35															
30				85					90					95	
				AGA					CAC					TAC	420
				AGA	Trp					Gly				TAC	420
40				AGA					CAC					TAC	420
40	Phe	Cys	Ala	AGA Arg	Trp 100	Glu	Val	Tyr	CAC His	Gly 105	Tyr	Val	Pro	TAC Tyr	
40	Phe TGG	Cys GGC	Ala CAA	AGA Arg GGG	Trp 100 ACC	Glu ACG	Val GTC	Tyr ACC	CAC His	Gly 105 TCC	Tyr TCT	Val GGC	Pro GGT	TAC Tyr	420
	Phe TGG Trp	Cys GGC	Ala CAA	AGA Arg GGG	Trp 100 ACC	Glu ACG Thr	Val GTC	Tyr ACC	CAC His	Gly 105 TCC	Tyr TCT Ser	Val GGC	Pro GGT	TAC Tyr	
40	Phe TGG	Cys GGC	Ala CAA	AGA Arg GGG	Trp 100 ACC	Glu ACG	Val GTC	Tyr ACC	CAC His	Gly 105 TCC	Tyr TCT	Val GGC	Pro GGT	TAC Tyr	
	TGG Trp 110	GGC Gly	Ala CAA Gln	AGA Arg GGG Gly	Trp 100 ACC Thr	ACG Thr 115	Val GTC Val	Tyr ACC Thr	CAC His GTT Val	Gly 105 TCC Ser	Tyr TCT Ser 120	Val GGC Gly	Pro GGT Gly	TAC Tyr GGC Gly	462
45	TGG Trp 110	Cys GGC Gly TCT	Ala CAA Gln GGT	AGA Arg GGG Gly	Trp 100 ACC Thr	ACG Thr 115	Val GTC Val	Tyr ACC Thr	CAC His GTT Val	Gly 105 TCC Ser	Tyr TCT Ser 120 GGT	Val GGC Gly TCT	Pro GGT Gly	TAC Tyr GGC Gly	
	TGG Trp 110	GGC Gly TCT Ser	Ala CAA Gln GGT	AGA Arg GGG Gly	Trp 100 ACC Thr	ACG Thr 115	Val GTC Val TCC Ser	Tyr ACC Thr	CAC His GTT Val	Gly 105 TCC Ser	Tyr TCT Ser 120 GGT	Val GGC Gly TCT Ser	Pro GGT Gly	TAC Tyr GGC Gly	462
45	TGG Trp 110	Cys GGC Gly TCT	Ala CAA Gln GGT	AGA Arg GGG Gly	Trp 100 ACC Thr	ACG Thr 115	Val GTC Val	Tyr ACC Thr	CAC His GTT Val	Gly 105 TCC Ser	Tyr TCT Ser 120 GGT	Val GGC Gly TCT	Pro GGT Gly	TAC Tyr GGC Gly	462

					TCT										546
	Gln	Leu	Thr	Gln	Ser	His	Lys	Phe	Leu	Ser	Thr	Ser	Val	Gly	
5	;		140					145					150		
	GAC	AGG	GTC	AGC	ATC	ACC	TGC	AAG	GCC	AGT	CAG	GAT	GTG	TAT	588
10	Asp	Arg	Val	Ser	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Val	Tyr	
10				155					160					165	
	AAT	GCT	GTT	GCC	TGG	TAT	CAA	CAG	AAA	CCA	GGA	CAA	TCT	CCT	630
15					Trp										
					170				Ī	175	·				
20	AAA	CTT	CTG	ATT	TAC	TCG	GCA	TCC	TCC	CGG	TAC	ACT	GGA	GTC	672
20	Lys	Leu	Leu	Ile	Tyr	Ser	Ala	Ser	Ser	Arg	Tyr	Thr	Gly	Val	
	180					185					190		Ī		
25	CCT	TCT	CGC	TTC	ACT	GGC	AGT	GGC	TCT	GGG	CCG	GAT	TTC	ACT	714
	Pro	Ser	Arg	Phe	Thr	${\tt Gly}$	Ser	Gly	Ser	Gly	Pro	Asp	Phe	Thr	
		195					200					205			
30															
					AGT										756
	Phe	Thr		Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Val	Tyr	
			210					215					220		
35															
					CAT										798
	Pne	Cys	GIn		His	Phe	Arg	Thr		Phe	Thr	Phe	Gly	Ser	
40				225					230					235	
	GGG	ACA	AAA	TTG	GAG	ATC	AAA	GCT	CTA	GAG	GGC	GGC	AGC	CTG	840
	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Ala	Leu	Glu	Gly	Gly	Ser	Leu	
45					240					245					
	GCC	GCG	CTG	ACC	GCG	CAC	CAG	GCC	TGC	CAC	CTG	CCG	CTG	GAG	882
50					Ala										- /-
.,	250					255					260				

										GGC					924
_	Thr		Thr	Arg	His	Arg	Gln	Pro	Arg	Gly	Trp	Glu	Gln	Leu	
5		265					270					275			
	GAG	CAG	TGC	GGC	TAT	CCG	GTG	CAG	CGG	CTG	GTC	GCC	CTC	TAC	966
10	Glu	Gln	Cys	Gly	Tyr	Pro	Val	Gln	Arg	Leu	Val	Ala	Leu	Tyr	
			280					285					290	-	
	CTG	GCG	GCG	CGA	CTG	TCA	TGG	AAC	CAG	GTC	GAC	CAG	GTG	ATC	1008
15										Val					-000
				295			-		300					305	
														505	
20	CGC	AAC	GCC	CTG	GCC	AGC	CCC	GGC	AGC	GGC	GGC	GAC	CTIC	ccc	1050
20										Gly					1030
	_				310			017	001	315	GLY	nop	Leu	GTA	
										313					
25	GAA	GCG	ልጥሮ	ccc	GAG	CAG	ccc	CAC	CAC	000	cam	ama			1092
										Ala					1092
	320			9	Olu	325	110	GIU	GIII	Ara	330	Leu	Ala	Leu	
						323					330				
30	ACC	CTTC	CCC	ccc	ccc	030	300	~~~							1134
															1134
	1111	335	Ата	ALG	Ala	GIU		GIU	Arg	Phe	Val	_	Gln	Gly	
35		333					340					345			
	100														
															1176
	mr	GIY		Asp	GIu	Ala	Gly		Ala	Asn	Ala	qaA	Val	Val	
40			350					355					360		
															1218
	Ser	Leu	Thr		Pro	Val	Ala	Ala	Gly	Glu	Cys	Ala	Gly	Pro	
45				365					370					375	
															1260
50	Ala	Asp	Ser	Gly	Asp	Ala	Leu	Leu	Glu	Arg	Asn	Tyr	Pro	Thr	
					380					385					

	GGC	GCG	GAG	THY	CTY	GGC	CAC	ccc	000		omo		-		1302
			Glu												
5	390				Lou	395		GIY	GIY	ASD			Pne	ser	
						333					400				
	ACC	CGC	GGC	ACG	CAG	AAC	TGG	ACG	GTG	GAG	ccc	CTIC	СПС	CAC	1344
	Thr	Arg	Gly	Thr	Gln	Asn	Trn	Thr	Val	Clu	250	T 011	7	CAG	1344
10		405					410	****	٠	Giu	Arg	415	rea	GIN	
							410					415			
	GCG	CAC	CGC	CAA	CTG	GAG	GAG	CGC	GGC	TAT	GTG	TTC	GTC	GGC	1386
15	Ala	His	Arg	Gln	Leu	Glu	Glu	Arg	Gly	Tyr	Val	Phe	Va1	Glv	
			420					425					430	2	
20	TAC	CAC	GGC	ACC	TTC	CTC	GAA	GCG	GCG	CAA	AGC	ATC	GTC	TTC	1428
20			Gly												
				435					440					445	
25	GGC	GGG	GTG	CGC	GCG	CGC	AGC	CAG	GAC	CTC	GAC	GCG	ATC	TGG	1470
			Val												
					450					455	-				
30															
30	CGC	GGT	TTC	TAT	ATC	GCC	GGC	GAT	CCG	GCG	CTG	GCC	TAC	GGC	1512
			Phe												
	460					465					470		-	-	
35															
	TAC	GCC	CAG	GAC	CAG	GAA	CCC	GAC	GCA	CGC	GGC	CGG	ATC	CGC	1554
	Tyr	Ala	Gln	Asp	Gln	Glu	Pro	Asp	Ala	Arg	Gly	Arg.	Ile	Arg	
40		475					480					485		_	
~															
	AAC	GGT	GCC	CTG	CTG	CGG	GTC	TAT	GTG	CCG	CGC	TCG	AGC	CTG	1596
	Asn	Gly	Ala	Leu	Leu	Arg	Val	Tyr	Val	Pro	Arg	Ser	Ser	Leu	
45			490					495					500		
															1638
50	Pro	Gly	Phe	Tyr	Arg	Thr	Ser	Leu	Thr	Leu	Ala	Ala	Pro	Glu	
~				505					510					515	

	GCG Ala	GCG Ala	GGC G1y	GAG	GTC Val	GAA Glu	CGG Arg	CTG	ATC	GGC	CAT	CCG	CTG	CCG	1680
5					520					525					
10	Leu 530	Arg	Leu	GAC Asp	GCC Ala	ATC Ile 535	Thr	GGC Gly	CCC Pro	GAG Glu	GAG Glu 540	Glu	GGC Gly	GGG Gly	1722
15	CGC Arg	CTG Leu 545	GAG Glu	ACC Thr	ATT I1e	CTC	Gly	TGG Trp	CCG Pro	CTG Leu	GCC	Glu	CGC Arg	ACC Thr	1764
20	GTG Val	GTG	ATT	CCC	TCG Ser	GCG Ala	550 ATC Ile	CCC Pro	ACC Thr	GAC Asp	CCG Pro	555 CGC Arq	AAC Asn	GTC Val	1806
25			560					565					570		1848
	Gly	Gly	Asp	Leu 575	Asp	Pro	Ser	Ser	Ile 580	Pro	Asp	Lys	Glu	Gln 585	1848
30	GCG Ala	ATC Ile	AGC Ser	GCC Ala	CTG Leu 590	CCG Pro	GAC Asp	TAC Tyr	Ala	Ser	CAG Gln	CCC Pro	GGC Gly	AAA Lys	1890
35	CCG	CCG	CGC	GAG		CTG	AAG	TAA		595	ac c	cccc	CCCT	~	1934
40	Pro 600	Pro	Arg	Glu	Asp	Leu 605	Lys								T32#
							CGGG		GGC	CATA	CAT	CAGG	TTTT		1984
45				M1 I	COAL		GAAT	10							2012

SEO ID NO:11

SEQUENCE TYPE: nucleotide with corresponding protein SEQUENCE LENGTH: 2012 bp MOLECULE TYPE: plasmid DNA ORIGINAL SOURCE ORGANISM: mouse/P.aeruginosa IMMEDIATE EXPERIMENTAL SOURCE: E.coli NAME OF CELL CLONE: ptwv215-51

FEATURES: from 1 to 63 bp

20

30

35

from 1 to 63 bp ompA signal peptide from 64 to 87 bp FLAG peptide and er

FLAG peptide and enterokinase cleavage

site

from 97 to 456 bp FWP51 heavy chain variable domain from 457 to 501 bp 15 amino acids linker sequence

from 502 to 822 bp FWP51 light chain variable domain from 826 to 1911 bp exotoxin A gene coding region

(coding for amino acids 252 to 613 of the

maturc exotoxin A)

from 1912 to 2012 bp 3' non-coding region of the exotoxin A gene

PROPERTIES: Fv heavy chain/light chain variable domain and exotoxin A fusion protein Fv(FWP51)-ETA binding to the c-crbB-2 protein

ATG AAA AAG ACA GCT ATC GCG ATT GCA GTG GCA CTG GCT GGT

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly

-30 -25 -20

TTC GCT ACC GTT GCG CAA GCT GAC TAC AAG GAC GAC GAC GAC GAC 84Phe Ala Thr Val Ala Gln Ala Asp Tyr Lys Asp Asp Asp -15-10

-5

AAG CTA GCT TCT CAG GTA CAA CTG CAG CAG TCT GGG GCT GAG 126 Lys Leu Ala Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu

1 5 10

	CTG	GTG	AGG	CCT	GGG	ACT	TCA	GTG	AAG	CTG	TCC	TGC	AAG	GCT	168
														Ala	
5				15					20			_	-	25	
	TCT	GAT	TAC	ACC	TTC	ACC	AGC	TAC	TGG	ATG	AAC	TGG	GTG	AAG	210
			Tyr												
10					30					35		-			
	CAG	AGG	CCT	GGA	CAA	GGC	CTT	GAA	TGG	ATT	GGT	ATG	ATT	GAT	252
15			Pro												
	40					45			-		50				
	CCT	TCA	GAC	AGT	GAA	ACT	CAA	TAC	AAT	CAA	ATG	TTC	AAG	GAC	294
20			Asp												
		55					60	-				65	-,, -,		
25	AAG	GCC	GCA	TTG	ACT	GTA	GAC	AAG	TCC	TCC	ААТ	ACA	GCC	TAC	336
			Ala												550
			70				-	75					80	-,-	
30	ATG	CAA	CTC	AGC	AGC	CTG	ACA	TCT	GAG	GAC	тст	GCG	GTC	ጥልጥ	378
			Leu												3,0
				85					90		DCI		vai	95	
35														,,	
	TAC	TGT	GCA	AAA	GGG	GGG	GCC	TCT	GGG	GAC	TGG	ጥልር	TPT/C	CAT	420
			Ala												120
					100	-			2	105		-1-	1116	rop	
40															
	GTC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTT	TCC	тст	GGC	GGT	462
			Gly												402
45	110					115					120		O ₁ y	OLY	
	GGC	GGT	TCT	GGT	GGC	GGT	GGC	TCC	GGC	GGT	GGC	CCT	пст	GAC	504
			Ser												204
50	_	125		-	-	-	130			1	1	135	JUL	, rob	
												-55			

	ATC	CAG	CTG	ACC	CAG	TCT	CCA	TCC	TCA	CTG	TCT	GCA	TCT	CTG	546
	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Leu	
5			140					145					150		
	GGA	GGC	GAA	GTC	ACC	ATC	ACT	TGC	AAG	GCA	AGC	CAA	GAC	ATT	588
10	Gly	Gly	Glu	Va1	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asp	Ile	
				155					160					165	
	AAG	AAG	TAT	ATA	GCT	TGG	TAC	CAA	CAC	AAG	CCT	GGA	AAA	AGT	630
15	Lys	Lys	Tyr	Ile	Ala	Trp	Tyr	Gln	His	Lys	Pro	Gly	Lys	Ser	
					170					175					
20														GGC	672
	Pro	Arg	Leu	Leu	Ile	His	Tyr	Thr	Ser	Val	Leu	Gln	Pro	Gly	
	180					185					190				
25			TCC												714
	Ile		Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Arg	Asp	Tyr	
		195					200					205			
30															
			AGC												756
	Ser	Phe	Ser	Ile	His	Asn	Leu	Glu	Pro	Glu	Asp	Ile	Ala	Thr	
			210					215					220		
35															
			TGT												798
	Tyr	Tyr	Cys		His	Tyr	Asp	Tyr	Leu	Tyr	Thr	Phe	Gly	Gly	
40				225					230					235	
			AAG												840
	GIĀ	Thr	Lys	Leu		Ile	Lys	Ala	Leu	Glu	Gly	Gly	Ser	Leu	
45					240					245					
	000		ome												
			CTG												882
50		Ala	Leu	Thr	Ala		Gln	Ala	Cys	His		Pro	Leu	Glu	
	250					255					260				

	ACT	TTC	ACC	CGT	CAT	CGC	CAG	CCG	CGC	GGC	TGG	GAA	CAA	CTG	924
	Thr	Phe	Thr	Arg	His	Arg	Gln	Pro	Arg	Gly	Trp	Glu	Gln	Leu	
5		265					270					275			
										CTG					966
10	Glu	Gln	Сув	Gly	Tyr	Pro	Val	Gln	Arg	Leu	Val	Ala	Leu	Tyr	
			280					285					290		
															1008
15	Leu	Ala	Ala		Leu	Ser	Trp	Asn	Gln	Val	Asp	Gln	Val	Ile	
				295					300					305	
	000														
20	700	AAC	GCC	CTG	GCC	AGC	ccc	GGC	AGC	GGC	GGC	GAC	CTG	GGC	1050
	ALG	ASII	АТа	Leu		Ser	Pro	Gly	Ser	Gly	Gly	Asp	Leu	Gly	
					310					315					
25	GAA	ccc	a mo	ccc	CAG	636	000				-				
										GCC Ala					1092
	320	ALU	116	ALG	GIU	325	Pro	GIU	GIn	Ala		Leu	Ala	Leu	
						323					330				
30	ACC	CTG	GCC	GCC	GCC	GAG	AGC	GAG	ccc	mmv.	CTC	ccc	C3.0	000	1134
	Thr	Leu	Ala	Ala	Ala	Glu	Ser	Glu	Ara	Phe	Val	724	CAG	01	1134
		335					340	- CIU	··· g	1116	Vai	345	GIII	GIĀ	
35												343			
	ACC	GGC	AAC	GAC	GAG	GCC	GGC	GCG	GCC	AAC	GCC	GAC	GTG	GTG	1176
										Asn					/0
40			350					355					360		
40															
															1218
	Ser	Leu	Thr	Cys	Pro	Val	Ala	Ala	Gly	Glu	Cys	Ala	Gly	Pro	
45				365					370					375	
															1260
50	Ala	Asp	Ser	Gly		Ala	Leu	Leu	Glu	Arg	Asn	Tyr	Pro	Thr	
					380					385					

	GGC	GCG	GAG	TTC	CTC	GGC	GAC	GGC	GGC	GAC	GTC	AGC	TTC	AGC	1302
5	Gly	Ala	Glu	Phe	Leu	Gly	Asp	Gly	Gly	Asp	Val	Ser	Phe	Ser	
	390					395					400				
	ACC	CGC	GGC	ACG	CAG	AAC	TGG	ACG	GTG	GAG	CGG	CTG	CTC	CAG	1344
10	Thr	Arg	Gly	Thr	Gln	Asn	Trp	Thr	Val	Glu	Arg	Leu	Leu	Gln	448
		405					410					415			
15	GCG	CAC	CGC	CAA	CTG	GAG	GAG	CGC	GGC	TAT	GTG	TTC	GTC	GGC	1386
	Ala	His	Arg	Gln	Leu	Glu	Glu	Arg	Gly	Tyr	Val	Phe	Val	Gly	
			420					425					430		
20															1428
	Tyr	His	Gly		Phe	Leu	Glu	Ala	Ala	Gln	Ser	Ile	Val	Phe	
				435					440					445	
25															
	GGC	GGG	GTG	CGC	GCG	CGC	AGC	CAG	GAC	CTC	GAC	GCG	ATC	TGG	1470
	GIY	Gly	Val	Arg		Arg	Ser	Gln	Asp	Leu	Asp	Ala	Ile	Trp	
					450					455					
30															
	CGC	GGT	TTC	TAT	ATC	GCC	GGC	GAT	CCG	GCG	CTG	GCC	TAC	GGC	1512
		GIA	Pne	Tyr	Ile		Gly	Asp	Pro	Ala	Leu	Ala	Tyr	Gly	
35	460					465					470				
	ma.c	000	03.0	~ ~											
	Tree	NI n	CAG	GAC	CAG	GAA	CCC	GAC	GCA	CGC	GGC	CGG	ATC	CGC	1554
40	TAT	475	GIII	nsp	GIII	GIU		Asp	Ala	Arg	Gly		Ile	Arg	
40		413					480					485			
	AAC	GGT	GCC	CTG	CTG	ccc	CEC.	mam.	ama	000	000	maa			1596
										Pro					1596
45			490	Deu	Deu	arg	vai	495	vaı	PLO	Arg	ser		Leu	
								400					500		
	CCG	GGC	TTC	TAC	CGC	ACC.	NCC.	CTC	7.00	cmc	000				1638
50										Leu					1038
-		×		505	- 3		- 02			Jeu	******	n1 d	1.10		
				202					510					515	

	GCG	GCG	GGC	GAG	GTC	GAA	CGG	CTG	ATC	GGC	CAT	CCG	CTG	CCG	1680
	Ala	Ala	Gly	Glu	Val	Glu	Arg	Leu	Ile	Glv	His	Pro	Len	Pro	
5					520		-			525					
	CTG	CGC	CTG	GAC	GCC	ATC	ACC	GGC	ccc	GAG	GAG	GAA	GGC	GGG	1722
	Leu	Arg	Leu	Asp	Ala	Ile	Thr	Glv	Pro	Glu	Glu	Glu	Glv	Glv	1.22
10	530					535		-			540		017		
	CGC	CTG	GAG	ACC	ATT	CTC	GGC	TGG	CCG	CTG	GCC	GAG	CGC	ACC	1764
15	Arg	Leu	Glu	Thr	Ile	Leu	Gly	Trp	Pro	Leu	Ala	Glu	Arq	Thr	
		545					550					555	-		
	GTG	GTG	ATT	CCC	TCG	GCG	ATC	CCC	ACC	GAC	CCG	CGC	AAC	GTC	1806
20	Val	Val	Ile	Pro	Ser	Ala	Ile	Pro	Thr	Asp	Pro	Arg	Asn	Val	
			560					565					570		
25	GGC	GGC	GAC	CTC	GAC	CCG	TCC	AGC	ATC	CCC	GAC	AAG	GAA	CAG	1848
	Gly	Gly	Asp	Leu	Asp	Pro	Ser	Ser	Ile	Pro	Asp	Lys	Glu	Gln	
				575					580					585	
30	GCG	ATC	AGC	GCC	CTG	CCG	GAC	TAC	GCC	AGC	CAG	CCC	GGC	AAA	1890
	Ala	Ile	Ser	Ala	Leu	Pro	Asp	Tyr	Ala	Ser	Gln	Pro	Gly	Lys	
					590					595					
35															
	CCG	CCG	CGC	GAG	GAC	CTG	AAG	TAA	CTG	CCGC	GAC	CGGC	CGGC	TC	1934
		Pro	Arg	Glu	Asp	Leu	Lys								
	600					605									
40															
	CCTT	CGCA	AGG A	GCCG	GCCI	T CT	CGGG	GCCI	' GGC	CATA	CAT	CAGG	TTTT	CC	1984
45	TGAT	GCCA	GC C	CAAT	CGAA	T AT	GAAT	TC							2012

50 Claims

- A recombinant antibody directed to the extracellular domain of the growth factor receptor c-erbB-2 comprising a heavy chain variable domain and a light chain variable domain of a monoclonal antibody.
- A recombinant antibody according to claim 1 wherein the heavy chain variable domain comprises a
 polypeptide of the formula
 FR₁-CDR_{HF}-FR₂-CDR_{2H}-FR₃-CDR_{3H}-FR₄ (I)
 wherein FR₁ is a polypeptide residue comprising 25-33 naturally occurring amino acids, FR₂ is a polypep-

tide residue comprising 12-16 naturally occurring amino acids, FR_3 is a polypeptide residue comprising 30-34 naturally occurring amino acids, FR_4 is a polypeptide residue comprising 6-13 naturally occurring amino acids, CDR_m is a polypeptide residue of the amino acid sequence 32 to 36 FSC in DNCA, CDR_m is a polypeptide residue of the amino acid sequence 32 to 36 FSC in DNCA, and CDR_m is a polypeptide residue of the amino acid sequence 50 to 67 of FSC in DNCA, and wherein the amino acid CS in the oxidized state forming SS-Dridges.

- 3. A recombinant antibody according to claim 2 wherein the heavy chain variable domain comprises a polypeptide of the amino acid sequence 2 to 120 of SEQ ID NO.4, wherein optionally one or more single amino acids within the amino acid sequences 2 to 31 (FR.), 37 to 50 (FR.), 68 to 99 (FR.), and/or 110 to 120 (FR.) are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-bridges.
- 4. A recombinant antibody according to claim 2 wherein the heavy chain variable domain comprises a polypeptide of the amino acid sequence 2 to ta 20 of SEQ ID NC-4, wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.
 - A recombinant antibody according to claim 1 wherein the light chain viable domain comprises a polypeptide of the formula

FR_cCDR_{IL}-FR_cCDR_{3L}-FR₆ (II)

wherein FR₆ is a polypeptide residue comprising naturally occurring amino acids, FR₇ is a polypeptide residue comprising 13-17 naturally occurring amino acids, FR₆ is a polypeptide residue comprising 30-34 naturally occurring amino acids, FR₆ is a polypeptide residue comprising naturally occurring amino acids, CDR_{IL} is a polypeptide residue of the amino acid sequence 159 to 169 of SEQ ID NO.4, CDR_{IL} is a polypeptide residue of the amino acid sequence 150 to 191 of SEQ ID NO.4, and CDR_{8L} is a polypeptide residue of the amino acid sequence 224 to 232 of SEQ ID NO.4, and wherein the amino acid Cys may be in the oxidzed state forming S-S-bridges.

 A recombinant antibody according to claim 5 wherein the light chain variable domain comprises a polypeptide of the amino acid sequence 138 to 241 of SEQ ID NO.4, wherein optionally one or more single amino acids within the amino acid sequences 138 to 158 (FRs.) 170 to 184 (FR.), 182 to 223 (FRs.), and/or 233 to 241 (FRs.) are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming 5.5-bridges.

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- A recombinant antibody according to claim 5 wherein the light chain variable domain comprises a polypep-5 tide of the amino acid sequence 138 to 241 of SEQ ID NO.4, wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.
 - A recombinant antibody according to claim 1 wherein the heavy chain variable domain comprises a
 polypeptide of the formula

FR,-CDR_{ur}-FR,-CDR_{ur}-FR_v-CDR_{ur}-FR_v (I) wherein FR₁ is a polypeptide residue comprising 25-33 naturally occurring amino acids, FR₂ is a polypeptide residue comprising 12-16 naturally occurring amino acids, FR₃ is a polypeptide residue comprising 30-34 naturally occurring amino acids, FR₄ is a polypeptide residue comprising 6-13 naturally occurring amino acids, CDR_{ur} is a polypeptide residue of the amino acid sequence 32 to 36 of SEQ ID NO:8, CDR_{ur} is a polypeptide residue of the amino acid sequence 51 to 67 of SEQ ID NO:8, and CDR_{ur} is a polypeptide residue of the amino acid sequence 100 to 110 of SEQ ID NO:8, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridged.

- 9. A recombinant antibody according to claim 8 wherein the heavy chain variable domain comprises a polypeptide of the amino acid sequence 2 to 121 of SEQ ID NO:8, wherein optionally one or more single amino acids within the amino acid sequences 2 to 31 (FR), 37 to 50 (FR), 88 to 99 (FR), and/or 111 to 121 (FR), are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.
- 10. A recombinant antibody according to claim 8 wherein the heavy chain variable domain comprises a polypeptide of the amino acid sequence 2 to 121 of SEQ ID NO.8, wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.

 A recombinant antibody according to claim 1 wherein the light chain variable domain comprises a polypeptide of the formula

FR₆-CDR₁₁-FR₇-CDR₂₁-FR₆-CDR₃₁-FR₆ (II)

wherein FR_s is a polypeptide residue comprising naturally occurring amino acids, FR_s is a polypeptide residue comprising 13-17 naturally occurring amino acids, FR_s is a polypeptide residue comprising naturally occurring amino acids, FR_s is a polypeptide residue comprising naturally occurring amino acids, CDR_s, is a polypeptide residue of the amino acid sequence 160 to 170 of SEQ ID NO.8, CDR_s, is a polypeptide residue of the amino acid sequence 180 to 192 of SEQ ID NO.8 and CDR_s, is a polypeptide residue of the amino acid sequence 225 to 232 of SEQ ID NO.8, and wherein the amino acid Cys may be in the oxidized state formino S-S-bridoss.

12. A recombinant antibody according to claim 11 wherein the light chain variable domain comprises a polypeptide of the amino acid sequence 137 to 241 of SEQ ID NO. 8, wherein optionally one or more single amino acids within the amino acid sequences 137 to 158 (FR_Q), 171 to 185 (FR_X), 193 to 224 (FR_Q), and/or 233 to 241 (FR_Q) are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.

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- 13. A recombinant antibody according to claim 11 wherein the light chain variable domain comprises a polypeptide of the amino acid sequence 137 to 241 of SEQ ID NO:8, wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.
 - 14. A recombinant antibody according to claim 1 which is a chimeric antibody consisting of a mouse heavy chain variable domain with the specificity for c-erbB-2 and a human heavy chain constant domain α, γ, δ, a or μ, and of a mouse light chain variable domain with the specificity for c-erbB-2 and a human light chain constant domain κ or λ, all assembled to give a functional antibody.
 - 15. A recombinant antibody according to claim 1 which is a single-chain antibody wherein the heavy chain variable domain and the light chain variable domain are linked by a polypeptide spacer group.
- 16. A single-chain recombinant antibody according to claim 15 further comprising an effector molecule and optionally comprising a peptide facilitating purification, a cleavage site and a peptide spacer.
 - 17. A single-chain recombinant antibody according to claim 16 wherein the effector molecule is an enzyme or a biologically active variant thereof.
- 18. A single-chain recombinant antibody according to claim 16 wherein the enzyme is alkaline phosphatase or a biologically active variant thereof.
 - 19. A single-chain recombinant antibody according to claim 16 wherein the effector molecule is a toxin or a biologically active variant thereof.
- A single-chain recombinant antibody according to claim 19 wherein the effector molecule is Pseudomonas
 exotoxin or a biologically active variant therof.
 - A single-chain recombinant antibody according to claim 16 wherein the heavy chain variable domain and the light chain variable domain are derived from a mouse monoclonal antibody selected from the group consisting of FRPS. FSP16. FWP51 and FSP77.
 - A single-chain recombinant antibody according to claim 21, further comprising an effector molecule or a biologically active variant thereof.
- 50 23. A single-chain recombinant antibody according to claim 21 wherein the heavy chain variable domain and the light chain variable domain are derived from the mouse monoclonal antibody FRP5.
 - 24. A single chain recombinant antibody according to claim 21 wherein the heavy chain variable domain and the light chain variable domain are derived from the mouse monoclonal antibody FWP51.
 - 25. A single-chain recombinant antibody according to claim 22 comprising the heavy chain variable domain of the mouse monocional antibody FRPs, the 15 amino acid polypeptide consisting of three repetitive subunits of G/FQ-IV-GV-GV-Ser, the light chain variable domain of the mouse monoclonal antibody FRPs, and

an enzyme or a toxin, or a biologically active variant thereof.

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- A single-chain recombinant antibody designated Fv(FRP5)-phoA according to claim 25 comprising a
 polypeptide of the amino acid sequence 2 to 690 of SEQ ID NO:5.
- A single-chain recombinant antibody designated Fv(FRP5)-ETA according to claim 25 comprising a
 polypeptide of the amino acid sequence 2 to 606 of SEQ ID NO: 10.
- 28. A single-chain recombinant antibody according to claim 22 comprising the heavy chain variable domain of the mouse monoclonal antibody FWP51, the 15 amino acid polypeptide consisting of three repetitive subunts of Gly-Gly-Gly-Gly-Ser, the light chain variable domain of the mouse monoclonal antibody FWP51, and an enzyme or a toxin, or a biologically active variant thereof.
- A single-chain recombinant antibody designated Fv(FWP51)-ETA according to claim 28 comprising a
 polypeptide of the amino acid sequence 2 to 606 of SEQ ID NO: 11.
- A mouse monoclonal antibody directed to the extracellular domain of the growth factor receptor c-erbB-2 selected from the group consisting of antibodies designated FRP5, FSP16, FSP77 and FWP51.
- A monoclonal antibody according to claim 30 designated FRP5.
 - 32. A monoclonal antibody according to claim 30 designated or FWP51.
 - 33. A method of manufacture of a recombinant antibody according to claim 1 or of a monoclonal antibody according to claim 30, characterized in that cells producing such an antibody are multiplied in vitro or in vivo and, when required, the obtained antibody is isolated.
- 34. A hybridoma cell secreting a monoclonal antibody according to claims 30.
- 35. A process for the preparation of a hybridoma cell line according to claim 34 secreting monoclonal antibodies directed to the extracellular domain of the growth factor receptor c-erbB-2, characterized in that a suitable mammal is immunized with purified c-erbB-2 protein, an antigenic carrier containing purified c-erbB-2 or with cells bearing c-erbB-2, antibody-producing cells of the immunized mammal are fused with cells of a suitable myeloma cell line, the hybrid cells obtained in the fusion are cloned, and cell clones secreting the desired antibodies are selected.
- 35 36. A recombinant DNA comprising an insert coding for a recombinant antibody according to claim 1.
 - 37. A recombinant DNA according to daim 36 comprising an insert coding for a heavy chain murine variable domain of a monoclonal antibody selected from the group consisting of antibodies FRP5, SP16, FSP77 and FWP51 or coding for an amino acid sequence homologous to said heavy chain variable domain.
- 38. A recombinant DNA according to claim 36 comprising an Insert coding for a light chain murine variable domain of a monoclonal antibody selected from the group consisting of antibodies FRPS, FGH, SPPY and FWPS1 or coding for an amin a cid secuence homologous to said light chain variable domain.
- 39. A recombinant DNA according to claim 36 which is a hybrid vector further comprising an origin of replication or an autonomously replicating sequence, one or more dominant marker sequences and, optionally, expression control sequences, sional sequences and additional restriction sites.
 - 40. A hybrid vector according to claim 39 comprising a Simian virus promoter and the mouse Ig H or L chain enhancer.
- 41. A process for the preparation of a DNA according to claim 36 comprising the steps of a) preparing murine DNA from the genome of a suitable hybridoma cell line and selecting the desired DNA coding for the variable heavy and/or light chain domains of the antibody with the desired specificity, b) preparing DNA coding for the desired signal sequence and/or preparing DNA coding for an effector molecule.
 - c) synthesizing DNA coding for the desired spacer group by chemical methods.
 - d) constructing recombinant genes encoding the recombiant antibodies by incorporating the DNA of

step a) and, optionally, b) and/or c) into appropriate hybrid vectors, e) transferring the obtained hybrid vectors into a recipient host cell or retrieving the DNA coding for the recomblinant genes and transferring the urflinked DNA into a recipient host cell, f) selecting and culturing the transformed host cell, and a) outclinally isolation the desired DNA.

- 42. A host cell transformed with a recombinant DNA according to claim 36.
- 43. A host cell according to claim 42 which is a cell of a strain of E. coli.
- 44. A process for the preparation of a transformed host cell according to claim 42 wherein suitable recipient cells are transformed with a hybrid vector comprising a DNA insert coding for a heavy chain murine variable domain and/or for a light chain murine variable domain of an antibody directed to the extracellular domain of the growth factor receptor c-erbB-2, an origin of replication or an autonomously replicating sequence, one or more dominant marker sequences and, optionally, expression control sequences, signal sequences and additional restriction sites, and the transformed cells are selected.
 - 45. Use of a recombinant antibody according to claim 1 for the qualitative and quantitative determination of the growth factor receptor c-erbB-2.
- Use of a monoclonal antibody according to claim 30 for the qualitative and quantitative determination of the growth factor receptor c-erbB-2.
 - 47. Use according to claim 45 comprising immunostaining of tissue sections with a solution containing the recombinant antibody comprising a detectable enzyme.
- 48. A test kit for the qualitative and quantitative determination of c-erbB-2 protein comprising a recombinant antibody according to claim 1 and/or a monoclonal antibody according to claim 30.
 - 49. A recombinant antibody according to claim 1 for use in the treatment of the human or animal body.
- 50. A monoclonal antibody according to claim 30 for use in the treatment of the human or animal body.
 - 51. A pharmaceutical composition for treating tumors over-expressing the growth factor receptor c-erb8-2 comprising a therapeutically effective amount of a recombinant antibody according to claim 1 or of a monoclonal antibody according to claim 30 and a pharmaceutically acceptable carrier.
 - 52. The use of a recombinant antibody according to claim 1 and/or a monoclonal antibody according to claim 30 for the manufacture of a pharmaceutical preparation.

Claims for the following Contracting State : ES

- Process for the preparation of a recombinant antibody directed to the extracellular domain of the growth
 factor receptor c-ertb-2 comprising a heavy chain variable domain and a light chain variable domain of
 a monoclonal antibody characterized in that cells producing such an antibody are multiplied in <u>vitro</u> or in
 <u>vivo</u> and, when required, the obtained antibody is isolated.
- Process according to claim 1 for the preparation of a recombinant antibody wherein the heavy chain variable domain comprises a polypeptide of the formula
 FR;-CDR_H-FR₂-CDR_S-FR₃-CDR_S-FR₄
 (I)
 - wherein FR₁ is a polypeptide residue comprising 25-33 naturally occurring amino acids, FR₂ is a polypeptide residue comprising 12-16 naturally occurring amino acids, FR₃ is a polypeptide residue comprising 30-34 naturally occurring amino acids, FR₃ is a polypeptide residue comprising e13 naturally occurring amino acids, CDR₁₁ is a polypeptide residue of the amino acid sequence 32 to 36 of SEQ ID NO.4, CDR₂₁ is a polypeptide residue of the amino acid sequence 51 to 67 SEQ ID NO.4 and CDR₂₁ is a polypeptide residue of the amino acid sequence 51 to 67 SEQ ID NO.4, and CDR₂₁ is a polypeptide residue of the amino acid sequence 51 to 67 SEQ ID NO.4 and cDR₂₁ is a polypeptide residue of the amino acid sequence 51 to 67 SEQ ID NO.4.
 - Process according to claim 2 for the preparation of a recombinant antibody wherein the heavy chain variable domain comprises a polypeptide of the amino acid sequence 2 to 120 of SEQ ID NO.4, wherein

optionally one or more single amino acids within the amino acid sequences 2 to 31 (FR₁), 37 to 50 (FR₂), 88 to 99 (FR₃), and or 110 to 120 (FR₂) are replaced by other amino acids or deleted, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.

- 4. Process according to claim 2 for the preparation of a recombinant antibody wherein the heavy chain variable domain comprises a polypeptide of the amino acid sequence 2 to 120 of SEQ ID NO:4, wherein the amino acid Cvs may be in the oxidized state forming S-S-bridges.
 - Process according to claim 1 for the preparation of a recombinant antibody wherein the light chain variable domain comprises a polypeptide of the formula

$$FR_6$$
- CDR_{11} - FR_7 - CDR_{21} - FR_6 - CDR_{32} - FR_9 (II)

wherein FR, is a polypeptide residue comprising naturally occurring amino acids, FR, is a polypeptide residue comprising 13-17 naturally occurring amino acids, FR, is a polypeptide residue comprising 30-34 naturally occurring amino acids, FR₈ is a polypeptide residue omprising naturally occurring amino acids, CDR₄, is a polypeptide residue of the amino acid sequence 159 to 169 of SEQ ID NO.4, O.DR₈, is a polypeptide residue of the amino acid sequence 158 to 191 of SEQ ID NO.4, and ODR₈, is a polypeptide residue of the amino acid sequence 224 to 232 of SEQ ID NO.4, and wherein the amino acid Cys may be in the oxidized state formino SS-b-irdoes.

- 6. Process according to claim 5 for the preparation of a recombinant antibody wherein the light chain variable domain comprises a polypeptide of the amino acid sequence 136 to 241 of SEQ. ID NO:4, wherein optionally one or more single amino acids within the amino acid sequences 138 to 158 (FR₂), 170 to 184 (FR₂), 192 to 223 (FR₂), and/or 233 to 241 (FR₂) are replaced by other amino acids or deleted, and wherein the amino acid Cvs may be in the oxidized state formino SS-briddees.
- Process according to claim 5 for the preparation of a recombinant antibody wherein the light chain variable
 domain comprises a polypeptide of the amino acid sequence 136 to 241 of SEQ ID NO:4, wherein the
 amino acid Cvs may be in the oxidized state forming 5-S-bridges.
- Process according to claim 1 for the preparation of a recombinant antibody wherein the heavy chain variable domain comprises a polypeptide of the formula

wherein FR, is a polypeptide residue comprising 25-33 naturally occurring amino acids, FR, is a polypeptide residue comprising 12-16 naturally occurring amino acids, FR, is a polypeptide residue comprising 30-34 naturally occurring amino acids, FR, is a polypeptide residue comprising 6-13 naturally occurring amino acids, CDR₂; is a polypeptide residue of the amino acid sequence 32 to 36 of SEQ ID NOS, act OR₂, is a polypeptide residue of the smino acid sequence 51 to 67 of SEQ ID NOS, and CDR₂, is a polypeptide residue of the amino acid sequence 10 to 110 of SEQ ID NOS, and wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.

- 40 9. Process according to claim 8 for the preparation of a recombinant antibody wherein the heavy chain variable domain comprises a polypeptide of the amino acid sequence 2 to 121 of SEQ ID NO.8, wherein optionally one or more single amino acids within the amino acid sequences 2 to 31 (FR), 37 to 50 (FR₂), 68 to 99 (FR₃), and/or 111 to 121 (FR₃) are replaced by other amino acids or deleted, and wherein the amino acid Cvs may be in the oxidized state formino 3-5-briddess.
 - 10. Process according to claim 8 for the preparation of a recombinant antibody wherein the heavy chain variable domain comprises a polypeptide of the amino acid sequence 2 to 121 of SEQ ID NO:8, wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.
- Process according to claim 1 for the preparation of a recombinant antibody wherein the light chain variable domain comprises a polypeptide of the formula

FR₄-CDR₁₁-FR₂-CDR₂₁-FR₈-CDR₃₁-FR₉ (II)

wherein FR, is a polypeptide residue comprising naturally occurring amino acids, FR, is a polypeptide residue comprising 13-17 naturally occurring amino acids, FR, is a polypeptide residue comprising 30-34 naturally occurring amino acids, FR₈ is a polypeptide residue comprising naturally occurring amino acids, CDR $_{1L}$ is a polypeptide residue of the amino acid sequence 160 to 170 of SEQ ID NO:8, CDR $_{2L}$ is a polypeptide residue of the amino acid sequence 180 to 120 of SEQ ID NO:8, and CDR $_{1L}$ is a polypeptide residue of the amino acid sequence 180 to 192 of SEQ ID NO:8, and CDR $_{1L}$ is a polypeptide residue of the amino acid sequence 180 to 192 of SEQ ID NO:8, and CDR $_{1L}$ is a polypeptide residue of the amino acid sequence 256 to 232 of SEQ ID NO:8, and wherein the similar acid Cys may be

in the oxidized state forming S-S-bridges.

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- 12. Process according to claim 11 for the preparation of a recombinant antibody wherein the light chain variable domain comprises a polypeptide of the amino acid sequence 137 to 241 of SEQ ID NO:8, wherein optionally one or more single amino acids within the amino acid sequences 137 to 159 [FRg.), 171 to 155 (FR), 130 to 224 (FRg.), and 224 (FRg.) are replaced by other amino acids or deleted, and wherein the amino acid Cvs may be in the oxidized state formino S-S-bridones.
- 13. Process according to claim 11 for the preparation of a recombinant antibody wherein the light chain variable domain comprises a polypeptide of the amino acid sequence 137 to 241 of SEQ ID NO.8, wherein the amino acid Cys may be in the oxidized state forming S-S-bridges.
- 14. Process according to claim 1 for the preparation of a recombinant antibody which is a chimeric antibody consisting of a mouse heavy chain variable domain with the specificity for c-orth-22 and a human leavy chain constant domain α, γ, δ, ε or μ, and of a mouse light chain variable domain with the specificity for c-orth-2 and a human light chain constant domain α, γ, δ, a or μ, and of a mouse light chain variable domain with α all assembled to give a functional antibody.
- 15. Process according to claim 1 for the preparation of a recombinant antibody which is a single-chain antibody wherein the heavy chain viable domain and the light chain variable domain are linked by a polypeptide spacer group.
- 16. Process according to claim 15 for the preparation of a single-chain recombinant antibody further comprising an effector notecute and optionally comprising a peptide facilitating purification, a cleavage site and a peptide spacer.
- 25 17. Process according to claim 16 for the preparation of a single-chain recombinant antibody wherein the effector molecule is an enzyme or a biologically active variant thereof.
 - 18. Process according to claim 16 for the preparation of a single-chain recombinant antibody wherein the enzyme is alkaline phosphatase or a biologically active variant thereof.
- Process according to claim 16 for the preparation of a single-chain recombinant antibody wherein the effector molecule is a toxin or a biologically active variant thereof.
- Process according to claim 19 for the preparation of a single-chain recombinant antibody wherein the effector molecule is Pseudomonas exotoxin or a biologically active variant therof.
 - Process according to claim 19 for the preparation of a single-chain recombinant antibody wherein the
 heavy chain variable domain and the light chain variable domain are derived from a mouse monoclonal
 antibody selected from the group consisting of FRP5, FSP16, FWP51 and FSP77.
- 40 22. Process according to claim 21 for the preparation of a single-chain recombinant antibody, further comprising an effector molecule or a biologically active variant thereof.
 - Process according to claim 21 for the preparation of a single-chain recombinant antibody wherein the heavy chain variable domain and the light chain variable domain are derived from the mouse monoclonal antibody FRP5.
 - Process according to claim 21 for the preparation of a single chain recombinant antibody wherein the heavy chain variable domain and the light chain variable domain are derived from the mouse monoclonal antibody FWP51.
- 25. Process according to claim 22 for the preparation of a single-chain recombinant antibody comprising the heavy chain variable domain of the mouse monoclonal antibody FRP5, the 15 amino acid polypeptide consisting of three repetitive subunits of Gly-Gly-Gly-Gly-Ser, the light chain variable domain of the mouse monoclonal antibody FRP5, and an enzyme or a toxin, or a biologically active variant thereof.
- 26. Process according to claim 25 for the preparation of a single-chain recombinant antibody designated Fv(FRP5)-phoA comprising a polypeptide of the amino acid sequence 2 to 690 of SEQID NO.5.

- Process according to claim 25 for the preparation of a single-chain recombinant antibody designated Fv(FRP5)-ETA comprising a polypeptide of the amino acid sequence 2 to 606 of SEQ ID NO: 10.
- 28. Process according to claim 22 for the preparation of a single-chain recombinant antibody comprising the heavy chain variable domain of the mouse monoclonal antibody FWP51, the 15 amino acid polypeptide consisting of three repetitive subunits of Gly-Gly-Gly-Gly-Ser, the light chain variable domain of the mouse monoclonal antibody FWP51, and an enzyme or a toxin, or a biologically active variant thereof.
- Process according to claim 28 for the preparation of a single-chain recombinant antibody designated Fv(FWP51)-ETA comprising a polypeptide of the amino acid sequence 2 to 606 of SEQ ID NO: 11.
 - 30. Process for the preparation of a mouse monoclonal antibody directed to the extracellular domain of the growth factor receptor o-erbb-2-selected from the group consisting of antibodies designated FRP5, FSP16, FSP71 and FWP51 characterized in that cells producing such an antibody are multiplied in <u>vitro</u> or in <u>vivo</u> and, when required, the obtained antibody is isolated.
- 31. A process according to claim 30 for the preparation of a monoclonal antibody designated FRP5.
- 32. A process according to claim 30 for the preparation of a monoclonal antibody designated or FWP51.
- 20 33. A process for the preparation of a hybridoma cell line secreting monoclonal antibodies directed to the extracellular domain of the growth factor receptor c-erble 2 selected from the grow consisting of antibodies designated FRP5, FSP16, FSP77 and FWP51, characterized in that a sultable mammal is immunized with purified c-erbB-2 protein, an antigenic carrier containing purified c-erbB-2 or with cells bearing c-erbB-2, antibody-producing cells of the immunized mammal are fused with cells of a sultable myeloma cell line, the hybrid cells obtained in the fusion are cloned, and cell clones secreting the desired antibodies are selected.
 - 34. A process for the preparation of a DNA comprising an insert coding for a recombinant antibody obtainable according to claim 1 comprising the steps of
- a) preparing murine DNA from the genome of a suitable hybridoma cell line and selecting the desired DNA coding for the variable heavy and/or light chain domains of the anibody with the desired specificity, b) preparing DNA coding for the desired signal sequence and/or preparing DNA coding for an effector molecule.
 - c) synthesizing DNA coding for the desired spacer group by chemical methods,
 - d) constructing recombinant genes encoding the recombiant antibodies by incorporating the DNA of step a) and, optionally, b) and/or c) into appropriate hybrid vectors.
 - e) transferring the obtained hybrid vectors into a recipient host cell or retrieving the DNA coding for the recombinant genes and transferring the unlinked DNA into a recipient host cell,
 f) selecting and culturing the transformed host cell, and
 - q) optionally isolating the desired DNA.

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- 35. A process according to claim 34 for the preparation of a DNA comprising an insert coding for a heavy chain murine variable domain of a monodonal antibody selected from the group consisting of antibodies FRP5, FSP16, FSP77 and FWP51 or coding for an amino acid sequence homologous to said heavy chain variable domain.
- 36. A process according to claim 34 for the preparation of a recombinant DNA comprising an insert coding for a light chain murine variable domain of a monodonal antibody selected from the group consisting of antibodies RPFs, FSP16, FSP77 and FWP51 or coding for an amino acid sequence homologous to said light chain variable domain.
- 37. A process according to claim 34 for the preparation of a recombinant DNA which is a hybrid vector further comprising an origin of replication or an autonomously replicating sequence, one or more dominant marker sequences and, optionally, expression control sequences, signal sequences and additional restriction sites.
- 38. A process according to claim 34 for the preparation of hybrid vector comprising a Simian virus promoter and the mouse Ig H or L chain enhancer.

- 39. A process for the preparation of a host cell transformed with a recombinant DNA obtainable according to claim 34 wherein suitable recipient cells are transformed with a hybrid vector comprising a DNA insert coding for a heavy chain murine variable domain and/or for a light chain murine variable domain of an antibody directed to the extracellular domain of the growth factor receptor c-erbB-2, an origin of replication or an autonomously replicating sequence, one or more dominant marker sequences and, optionally, expression control sequences, signal sequences and additional restriction sites, and the transformed cells are selected.
- A process for the preparation of a host cell according to claim 42 wherein the host cell is a cell strain of <u>E. coli.</u>



EUROPEAN SEARCH REPORT

Application Number

92 81 0056

Category	Citation of document with indication of relevant passages	a, where appropriate,	Relevant to claim	CLASSIFICATION OF TH APPLICATION (Int. CL5)					
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